

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2005, 09:44:30 ; Search time 72 Seconds
(without alignments)
1058.219 Million cell updates/sec

Title: US-10-077-406-1
Perfect score: 1133
Sequence: 1 SQQAVPPYASENQTCRDOE.....QSDTTCKNPLEPLPPMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	197	2	Aaw23220 Extracell
2	1133	100.0	197	2	Aay31326 Human lym
3	1133	100.0	197	8	Ado43009 Lymphotox
4	1133	100.0	305	8	Adj67643 Human ova
5	1133	100.0	435	6	Abp96137 Human TNF
6	1133	100.0	435	6	Abp96137 Human TNF
7	1133	100.0	435	6	Abp96137 Human TNF
8	1133	100.0	435	7	Abp96137 Human TNF
9	1133	100.0	435	7	Abp96137 Human TNF
10	1133	100.0	435	8	Abp96137 Human TNF
11	1133	100.0	435	8	Abp96137 Human TNF
12	1133	100.0	435	8	Abp96137 Human TNF
13	1133	100.0	435	8	Abp96137 Human TNF
14	1133	100.0	435	8	Abp96137 Human TNF
15	1129	99.6	399	6	Abp96136 Human TNF
16	1129	99.6	399	6	Abp96136 Human TNF
17	1129	99.6	410	8	Abm83612 Human ova
18	1122	99.0	293	8	Adp81157 Protein o
19	1122	99.0	635	8	Adj67641 Human ova
20	1122	99.0	635	8	Adj67641 Human ova
21	1108	97.8	416	7	Adc42856 REMAP pro
22	1091	96.3	361	8	Adj67637 Human ova
23	1091	96.3	361	8	Adj67637 Human ova
24	987	87.1	170	6	Ada49700 Extracell
25	981	86.6	170	7	Adl17745 human Lym

26	970	85.6	172	8	ADJ56818	Adj56818 Human LTB
27	771	68.0	402	7	ABM85508	Abm85508 Mouse pro
28	771	68.0	415	4	ABM36700	Abm36700 Human tum
29	771	68.0	415	6	ABP96138	Abp96138 Mouse lym
30	771	68.0	415	7	ADP18289	Adp18289 TL5 recep
31	771	68.0	415	8	ADJ96157	Adj96157 Human LTB
32	756	66.7	166	8	ADP81159	Adp81159 Protein o
33	456	40.2	77	2	AAW94642	Aaw94642 TNF-R ext
34	456	40.2	77	4	ABM69194	Abm69194 Human TNF
35	381.5	33.7	305	5	ABP41926	Abp41926 Human ova
36	381.5	33.7	305	5	ADP81160	Adp81160 Protein o
37	315	27.8	518	2	AAK51003	Aak51003 Sequence
38	311.5	27.5	659	6	ABJ37103	Abj37103 Concatame
39	311.5	27.5	659	8	ADQ79910	Adq79910 Human tum
40	309	27.3	461	2	AAW72504	Aaw72504 p75 Tumou
41	307	27.1	720	6	ABJ37101	Abj37101 Concatame
42	307	27.1	720	8	ADQ79906	Adq79906 Human tum
43	305	26.9	225	3	AAJ77463	Aaj77463 Primate p
44	305	26.9	225	6	AAO26526	Aao26526 Human tum
45	305	26.9	227	4	AAB66981	Aab66981 Tnfr2 pro

ALIGNMENTS

RESULT 1

AAW23220

ID AAW23220 standard; protein; 197 AA.

XX AC AAW23220;

XX AC AAW23220;

DT 29-OCT-1997 (first entry)

XX DE Extracellular domain of human lymphotoxin beta receptor.

XX KW Human, lymphotoxin beta; receptor; blocking agent; extracellular;

XX KW ligand binding; domain; treatment; Th1 cell; immune response; delayed;

XX KW hypersensitivity; contact; tuberculin; granulomatous; graft versus host;

XX KW disease; organ rejection; autoimmune; disorder; multiple sclerosis;

XX KW insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia;

XX KW psoriasis; Listeria; Toxoplasma; infection; Mycobacterium; abnormal;

XX KW lymphoid organ; development.

XX OS Homo sapiens.

XX PN WO9703687-A1.

XX PD 06FEB1997.

XX 19-JUL-1996; 96WO-US012010.

XX 21-JUL-1995; 95US-00505606.

XX (BIOJ) BIOGEN INC.

XX Browning JL, Benjamin CD, Hochman PS;

XX WPI, 1997-132373/12.

XX Compositions comprising lymphotoxin-beta receptor blocking agent - used

XX to treat autoimmune diseases, e.g. sclerosis, insulin-dependent

XX diabetes, etc.

XX Example 1; Page 55-56; 76pp; English.

XX The present sequence, a human lymphotoxin beta receptor (LT-beta-R)

XX blocking agent, comprises the extracellular ligand binding domain of the

XX human LT-beta-R up to the transmembrane region. It can be used to treat a

XX Th1 cell mediated immune response which contributes to a delayed type

XX hypersensitivity reaction, preferably contact, tuberculin type or

XX granulomatous hypersensitivity, graft versus host disease, organ

XX rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin

XX dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can

Lee, B.
10/077406
Seq. ID 1

CC also be used to treat conditions exacerbated by the activities of Th-1
 CC type cytokines, or Listeria, Toxoplasma or Mycobacterium infection. Its
 CC ability to selectively or partially block the LT-beta-R pathway may be
 CC useful in the treatment of abnormal lymphoid organ development associated
 CC with misexpression or overexpression of signalling by the LT-beta-R
 CC pathway. The present LT-beta-R blocking agent is capable of selectively
 CC inhibiting Th1, but not Th2 cell dependent immune effector mechanisms. As
 CC Th1 cytokines can inhibit Th2 cell dependent responses, the present LT-
 CC beta-R blocking agent may also indirectly stimulate certain Th2 cell
 CC dependent responses which are normally inhibited by Th1 induced
 CC cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are
 CC expected to be suitable starting doses for optimising treatment
 XX
 SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 1.2e-78;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQQAVPPYASENOTCRDOEKEYEYEPQHRICCSRCPPGTYVSAKSRIKDTVCATCAENS 60
 DB 1 SQQAVPPYASENOTCRDOEKEYEYEPQHRICCSRCPPGTYVSAKSRIKDTVCATCAENS 60
 QY 61 YNEHNYLTICQLCRPCDPVMGLEEIAPTCKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 DB 61 YNEHNYLTICQLCRPCDPVMGLEEIAPTCKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
 DB 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
 QY 181 TTCKNPLEPLPPMSGT 197
 DB 181 TTCKNPLEPLPPMSGT 197

RESULT 2
 AAY31326
 ID AAY31326 standard; peptide; 197 AA.

XX AAY31326;
 AC
 XX
 XX
 DT 04-OCT-1999 (first entry)
 DE Human lymphotoxin (LT)beta-receptor extracellular region.
 XX
 KW Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;
 KW immune system; tumour; follicular lymphoma; extracellular domain; human.
 OS Homo sapiens.
 XX
 XX WO9938525-A1.
 XX
 PD 05-AUG-1999.
 XX
 XX 29-JAN-1999; 99WO-US001928.
 XX
 XX 30-JAN-1998; 98US-0073112P.
 PR 02-FEB-1998; 98US-0073410P.
 XX
 XX (BIOJ) BIOGEN INC.
 XX
 XX Browning J, Thorbecke J, Tsiagbe V;
 XX WPI; 1999-469242/39.
 XX
 XX New method of treating follicular lymphomas by inhibiting interaction
 PT between lymphotoxin-beta and its receptor.
 XX
 XX Example 1; Page 25-26; 31pp; English.
 PS
 XX The invention provides a method for arresting or reducing, severity of
 CC effects of a tumour by administration of a composition which inhibits the

CC interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor
 CC of the interaction between LT-beta and its receptor can be administered
 CC for altering the survival or maintenance of follicular dendritic cells in
 CC a subject and for altering the architecture of the organs of the immune
 CC system. The method is useful for treating tumours, specifically
 CC follicular lymphomas. It offers an alternative therapy for those with
 CC tumours resistant to traditional chemotherapy. The present sequence
 CC represents the extracellular region of the human LTbeta-receptor and
 CC comprises the ligand binding domain
 XX
 SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 1.2e-78;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQQAVPPYASENOTCRDOEKEYEYEPQHRICCSRCPPGTYVSAKSRIKDTVCATCAENS 60
 DB 1 SQQAVPPYASENOTCRDOEKEYEYEPQHRICCSRCPPGTYVSAKSRIKDTVCATCAENS 60
 QY 61 YNEHNYLTICQLCRPCDPVMGLEEIAPTCKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 DB 61 YNEHNYLTICQLCRPCDPVMGLEEIAPTCKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
 DB 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
 QY 181 TTCKNPLEPLPPMSGT 197
 DB 181 TTCKNPLEPLPPMSGT 197

RESULT 3
 ADO43009
 ID ADO43009 standard; protein; 197 AA.

XX ADO43009;
 AC
 XX
 XX 29-JUL-2004 (first entry)
 XX
 DE Lymphotoxin-beta receptor (soluble form).
 XX
 KW Human; Lymphotoxin-beta receptor; receptor; immunomodulator;
 KW antirheumatic; antiarthritic; antidiabetic; urologic; dermatological.
 XX
 OS Homo sapiens.
 XX
 XX WO2004039329-A2.
 XX
 PD 13-MAY-2004.
 XX
 XX 31-OCT-2003; 2003WO-US034813.
 XX
 XX 31-OCT-2002; 2002US-0422588P.
 PR
 XX (BIOJ) BIOGEN INC.
 PA
 PI Gommerman J, Browning JL;
 XX
 XX WPI; 2004-376051/35.
 XX
 XX Treating an animal having an immunological renal disorder or
 PT glomerulonephritis comprises administering to the animal a composition
 PT comprising an inhibitor of the lymphotoxin (LT) pathway.
 XX
 XX Claim 7; SEQ ID NO 1; 47pp; English.

XX The present is the protein sequence of a soluble lymphotoxin-beta
 CC receptor (LTBR) comprising the extracellular domain of LTBR that is
 CC capable of binding lymphotoxin (LT) specifically. The invention provides
 CC methods for treating immunological disorders, including pathologies
 CC associated with immunoglobulin deposits in the kidneys. It is based in

CC part on the discovery that inhibition of the LT pathway with a soluble
CC form of LTBR leads to amelioration of lupus-like disease in BAFF-
CC transgenic mice. It is also based in part on the discovery that renal
CC dysfunction in BAFF-transgenic mice is associated with accumulation of
CC IgA and IgG immune complexes in the kidneys. Methods are provided for
CC treating immunological diseases, including diseases caused by
CC dysregulated production of immunoglobulins by B cells, including
CC dysregulated production of IgA or IgG. Compositions comprising inhibitors
CC of the LT pathway are used to prevent or treat pathologies associated
CC with renal dysfunction accompanied by immunoglobulin deposits, including
CC glomerulonephritis. Suitable inhibitors include soluble forms of LTBR.
CC The methods are useful for treating an immunological renal disorder, e.g.
CC systemic lupus erythematosus, Sjorgen's syndrome, rheumatoid arthritis,
CC insulin-dependent diabetes mellitus, chronic hepatitis, Henoch-Schonlein
CC purpura, IgA nephropathy or glomerulonephritis.

XX Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 60
DB 1 SQQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 60
QY 61 YNEHWNLYTICQLCRPCDPVWGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 61 YNEHWNLYTICQLCRPCDPVWGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
QY 121 CPPGTEAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 121 CPPGTEAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
QY 181 TTCKNPLEPLPPMSGT 197
DB 181 TTCKNPLEPLPPMSGT 197

RESULT 4
ADJ67643
ID ADJ67643 standard; protein; 305 AA.
XX
XX ADJ67643;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human ovarian specific polypeptide SEQ ID NO:357.
DE
DE human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;
KW ovarian cancer; immune response; cancer.
XX
XX Homo sapiens.
XX
XX WO2004013311-A2.
XX
XX 12-FEB-2004.
XX
XX 06-AUG-2003; 2003WO-US024669.
XX
XX 06-AUG-2002; 2002US-0401469P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Salceda S, Liu C, Sun Y, Turner LR;
PI
XX WPI; 2004-169331/16.
XX
XX New ovarian specific nucleic acid, useful in identifying, diagnosing,
PT monitoring, staging, imaging and treating ovarian cancer and non-
PT cancerous disease states in ovarian tissue.
XX
XX Claim 12; SEQ ID NO 357; 586pp; English.

XX The invention relates to novel isolated ovarian specific nucleic acid
CC molecules and the polypeptides encoded by them. A protein of the
CC invention has cytostatic and immunostimulant activity. A nucleic acid of
CC the invention may have a use as a vaccine, and in gene therapy. The
CC nucleic acid molecule or polypeptide, antibody or kit is useful in
CC identifying, diagnosing, monitoring, staging, imaging and treating
CC ovarian cancer and non cancerous disease states in ovarian tissue and in
CC inducing an immune response against the ovarian cancer cell. The
CC sequences shown in ADJ67535-ADJ67682 represent ovarian specific
CC polypeptides of the invention.

XX Sequence 305 AA;

Query Match 100.0%; Score 1133; DB 8; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 60
DB 28 SQQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVWGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLYTICQLCRPCDPVWGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPGTEAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 5
ABP96137
ID ABP96137 standard; protein; 435 AA.
XX
XX ABP96137;
XX
XX 09-MAY-2003 (first entry)
XX
XX Human TNF receptor 2 related protein/LTRbeta SEQ ID NO:19.
XX
XX Human; tumour necrosis factor receptor 2 related protein variant;
KW TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;
KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
KW asthma; ulcerative colitis.
XX
XX Homo sapiens.
XX
XX WO2003012037-A2.
XX
XX 13-FEB-2003.
XX
XX 24-JUL-2002; 2002WO-US023684.
XX
XX 27-JUL-2001; 2001US-00917372.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Lal PG, Warren BA;
XX
XX WPI; 2003-256445/25.
XX
XX New cDNA, useful for preparing a composition for treating a disease or
PT condition associated with increased TNF signaling e.g., cancer of the
PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
PT rheumatoid arthritis, asthma.
XX
XX Disclosure; Fig 2A-C; 64pp; English.

CC The present invention describes human tumour necrosis factor receptor 2
CC related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic
CC and immunosuppressive activities, and can be used in gene therapy. The
CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
CC for treating a disease or condition associated with increased TNF
CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
CC arthritis, asthma or ulcerative colitis. The present sequence represents
CC a human TNFR2 related protein/TNFR2beta amino acid sequence, which is given
CC in comparison with human TNFR2PV in the exemplification of the present
CC invention
XX

SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.8e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAQVPPYASENQTCDQKEYYEPOHRIICCSRCPPGTYVSAKCSRIKDTVCATCAENS 60
DB 28 SQQAQVPPYASENQTCDQKEYYEPOHRIICCSRCPPGTYVSAKCSRIKDTVCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVWGLEIEAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLYTICQLCRPCDPVWGLEIEAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 6
ABR40220
ID ABR40220 standard; protein; 435 AA.
AC ABR40220;
XX

12-JUN-2003 (first entry)

Human genoxin.

XX Human; genoxin; antiarteriosclerotic; antidiabetic; hypotensive;
KW antilipaeamic; anorectic; immunomodulator; cytostatic; anti-HIV;
KW antiinflammatory; cardiant; cerebroprotective; gene therapy;
XX tumour necrosis factor receptor; TNFR; body mass; weight loss; obesity.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..30
FT /label= Signal_peptide
FT Protein 31..435
FT Domain /label= Mature_genoxin
FT Domain 31..227
FT Domain /label= Extracellular_domain
FT Domain 228..248
FT Domain /label= Transmembrane_domain
FT Domain 249..435
FT /label= Intracellular_domain

XX WO2003011322-A1.

XX 13-FEB-2003.

XX 31-JUL-2002; 2002WO-IB003417.

XX 02-AUG-2001; 2001US-0309917P.

XX (GEST) GENSET SA.

XX PI Lucas J, Dialynas D, Briggs K;
XX WPI; 2003-256417/25.
DR N-PSDB; ABZ99578.
XX Screening for an agonist or antagonist of Genoxin activity, useful for
PT preventing or treating metabolic disorders, comprises contacting Genoxin
FT polypeptide with a test compound and determining binding.
XX Example 10; Page 33-34; 37pp; English.

XX The invention relates to a novel method for screening for an agonist or
CC antagonist of Genoxin activity. The agonists/antagonists of the invention
CC have antiarteriosclerotic, antidiabetic, hypotensive, antilipaeamic,
CC anorectic, immunomodulator, cytostatic, anti-HIV, antiinflammatory,
CC cardiant, and cerebroprotective activity. The polypeptides of the
CC invention may have a use in gene therapy, and act as tumour necrosis
CC factor receptor (TNFR) agonists. The method is used to screen for an
CC agonist or antagonist of Genoxin. The method is useful in metabolic
CC research, particularly, in discovering compounds that modulate Genoxin
CC activity or that reduce or increase body mass and maintain weight loss,
CC and in preventing or treating obesity-related diseases or disorders such
CC as hyperlipidaemia, atherosclerosis, heart disease, stroke, insulin-
CC resistant diabetes or hypertension, or for preventing or treating
CC disorders associated with excessive weight loss, such as cachexia, cancer
CC -related weight loss, acquired immunodeficiency syndrome (AIDS)-related
CC weight loss, chronic inflammatory disease-related weight loss, or
CC anorexia. The present sequence represents the human genoxin of the
CC invention

XX Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.8e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAQVPPYASENQTCDQKEYYEPOHRIICCSRCPPGTYVSAKCSRIKDTVCATCAENS 60
DB 28 SQQAQVPPYASENQTCDQKEYYEPOHRIICCSRCPPGTYVSAKCSRIKDTVCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVWGLEIEAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLYTICQLCRPCDPVWGLEIEAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 7

ABU89821
ID ABU89821 standard; protein; 435 AA.
XX

ABU89821;

XX 10-JUL-2003 (first entry)

XX TNF-receptor associated factor 5 (TRAF5) interacting protein #1.

XX Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;

XX TNF-receptor associated factor 5 interacting protein;

XX tumour necrosis factor associated factor 5 interacting protein;

XX TRAF5 interacting protein.

XX Homo sapiens.

XX WO2003031571-A2.

PD 17-APR-2003.
XX
PP 02-OCT-2002; 2002WO-US031357.
XX
XX 05-OCT-2001; 2001US-0327454P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 25-JUN-2002; 2002US-0391342P.
PR 01-OCT-2002; 2002US-00262445.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
PI Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;
PI Mezes PS, Millet I, Ooi CE, Patturajan M, Rieger DK, Spytek KA;
PI Taupier RJ, Zerhusen BD, Zhong H, Zhong M;
XX
XX WPI; 2003-381704/36.
DR N-PSDB; ACA90237.
XX
XX New DAPK3 polypeptide, useful for preparing a composition for treating or
PT preventing e.g., cancer.
XX
XX Example 20F; Page 240; 253pp; English.
XX
XX The invention describes an isolated polypeptide comprising any of 33 90-
CC 1273 amino acid sequences (I) given in the specification or its mature
CC form, a sequence that is at least 95 % identical to (I), or a sequence
CC comprising one or more conservative substitutions in the amino acid
CC sequence of (I). The polypeptide is useful for preparing a composition
CC for treating or preventing e.g. cancer. This is the amino acid sequence
CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
CC interacting protein associated with the identification of novel human
CC proteins and their functions
XX
XX Sequence 435 AA;
SQ
Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.8e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQQAVPPYASENQTCDQKEYYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS 60
DB 28 SQQAVPPYASENQTCDQKEYYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVWGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLYTICQLCRPCDPVWGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAEELKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSD 180
DB 148 CPPGTEAEELKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224
RESULT 8
ADF50693
ID ADF50693 standard; protein; 435 AA.
XX
AC ADF50693;
XX
DT 12-FEB-2004 (first entry)

XX
DE
XX
KW Human lymphotoxin-beta protein.
KW human; lymphotoxin-beta; allograft rejection; graft versus host disease;
KW Herpesvirus entry mediator; HVEM; LIGHT; immunosuppressive; cyclosporin;
KW corticosteroid; antiproliferative; HVEM-LIGHT inhibitor; cytokine;
KW TNF-family ligand; delayed hypersensitivity; atrophic gastritis;
KW thyroiditis; allergic encephalomyelitis; autoimmune haemolytic anaemia;
KW sympathetic ophthalmia; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis;
KW immune disorder.
XX
OS Homo sapiens.
XX
PN EP1336619-A2.
XX
XX 20-AUG-2003.
XX
XX 18-FEB-2003; 2003EP-00003651.
XX
XX 19-FEB-2002; 2002US-0358463P.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Fraser CC, Hancock W;
XX
XX WPI; 2003-665560/63.
DR N-PSDB; ADF50692.
XX
XX A composition containing an immunosuppressive agent and a molecule which
PT inhibits binding of Herpesvirus entry mediator to the tumor necrosis
PT factor superfamily member LIGHT is useful to treat or prevent immune
PT disorders.
XX
XX Disclosure; SEQ ID NO 17; 52pp; English.
XX
XX This invention relates to a novel method for suppressing immune disorders
CC such as allograft rejection or graft versus host disease. Specifically,
CC it comprises a Herpesvirus entry mediator (HVEM)-LIGHT inhibitor and an
CC immunosuppressive agent to prepare a pharmaceutical composition that can
CC treat or prevent an immune disorder. The present invention describes the
CC immunosuppressive agent as, for example, a cyclosporin, corticosteroid or
CC an antiproliferative agent, whereas the HVEM-LIGHT inhibitor can be an
CC antibody or any molecule including dominant negative proteins (such as
CC soluble HVEM proteins) that can disrupt binding between the cytokine
CC LIGHT (a TNF-family ligand also known as Tango-69, which is expressed by
CC activated T cells) and its receptor HVEM. As such, these compositions can
CC be used for the treatment of delayed hypersensitivity, atrophic
CC gastritis, thyroiditis, allergic encephalomyelitis, autoimmune haemolytic
CC anaemia, sympathetic ophthalmia, systemic lupus erythematosus, rheumatoid
CC arthritis, multiple sclerosis or myasthenia gravis. This polypeptide is
CC the human lymphotoxin-beta protein sequence, a dominant negative form of
CC a receptor to which LIGHT binds other than HVEM, used in an
CC exemplification of the invention.
XX
XX Sequence 435 AA;
SQ
Query Match 100.0%; Score 1133; DB 7; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.8e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQQAVPPYASENQTCDQKEYYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS 60
DB 28 SQQAVPPYASENQTCDQKEYYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVWGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLYTICQLCRPCDPVWGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAEELKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSD 180
DB 148 CPPGTEAEELKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 9
 ABM85509
 ID ABM85509 standard; protein; 435 AA.
 XX
 AC
 XX ABM85509;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human protein sequence hCP41584.
 XX
 KW Cytostatic; carcinoma; lymphoma; cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003073826-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 28-FEB-2003; 2003WO-US006235.
 XX
 PR 01-MAR-2002; 2002US-0008192.
 XX
 PA (SAGR-) SAGRES DISCOVERY.
 XX
 PI Morris DW;
 XX
 DR WPI; 2003-328604/31.
 XX
 PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
 PT comprises a nucleotide sequence.
 XX
 PS Claim 5; SEQ ID NO 942; Opp; English.
 XX
 CC The present invention relates to novel DNA and protein sequences which
 CC are associated with carcinomas. The sequences are useful for: (i) for
 CC screening drug candidates; (ii) for screening of bioactive agent capable
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
 CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
 CC determining Carcinoma Associated (CA) gene copy number. In addition, the
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
 CC carcinoma including lymphoma. The present sequence is one such CAP. Note:
 CC this patent is an equivalent to basic patent US2002182586A1, for which no
 CC sequence data was published
 XX
 SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 7; Length 435;
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCRDQKEYEYEPQHRICCSRCPPGTYYSAKCSRIKDTVCATCAENS 60
 DB 28 SQQAVPPYASENQTCRDQKEYEYEPQHRICCSRCPPGTYYSAKCSRIKDTVCATCAENS 87

QY 61 YNEHWNLYITICQLCRPCDPVPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 DB 88 YNEHWNLYITICQLCRPCDPVPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTEAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSD 180
 DB 148 CPPGTEAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 11

DB 208 TTCKNPLEPLPPMSGT 224

RESULT 10
 ADJ67639
 ID ADJ67639 standard; protein; 435 AA.
 XX
 AC ADJ67639;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human ovarian specific polypeptide SEQ ID NO:353.
 XX
 KW human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;
 KW ovarian cancer; immune response; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2004013311-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 06-AUG-2003; 2003WO-US024669.
 XX
 PR 06-AUG-2002; 2002US-0401469P.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Macina RA, Salceda S, Liu C, Sun Y, Turner LR;
 XX
 DR WPI; 2004-169331/16.
 XX
 PT New ovarian specific nucleic acid, useful in identifying, diagnosing,
 PT monitoring, staging, imaging and treating ovarian cancer and non-
 PT cancerous disease states in ovarian tissue.
 XX
 PS Claim 12; SEQ ID NO 353; 586pp; English.
 XX
 CC The invention relates to novel isolated ovarian specific nucleic acid
 CC molecules and the polypeptides encoded by them. A protein of the
 CC invention has cytostatic and immunostimulant activity. A nucleic acid of
 CC the invention may have a use as a vaccine, and in gene therapy. The
 CC nucleic acid molecule or polypeptide, antibody or kit is useful in
 CC identifying, diagnosing, monitoring, staging, imaging and treating
 CC ovarian cancer and non cancerous disease states in ovarian tissue and in
 CC inducing an immune response against the ovarian cancer cell. The
 CC sequences shown in ADJ67535-ADJ67682 represent ovarian specific
 CC polypeptides of the invention.
 XX
 SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 8; Length 435;
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCRDQKEYEYEPQHRICCSRCPPGTYYSAKCSRIKDTVCATCAENS 60
 DB 28 SQQAVPPYASENQTCRDQKEYEYEPQHRICCSRCPPGTYYSAKCSRIKDTVCATCAENS 87

QY 61 YNEHWNLYITICQLCRPCDPVPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 DB 88 YNEHWNLYITICQLCRPCDPVPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTEAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSD 180
 DB 148 CPPGTEAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 11

ABM81345	DB	88	YNEHNYLTICQLCRPCDPVWGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD	147
ID	ABM81346	AC	standard; protein; 435 AA.	
XX	ABM81346;	AC		
XX	18-NOV-2004	(first entry)		
XX	Tumour-associated antigenic target (TAT) polypeptide PRO2622, SEQ:3477.			
XX	Tumour-associated antigenic target; TAT; human; overexpression; cancer;			
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;			
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;			
KW	central nervous system cancer; bladder cancer; pancreatic cancer;			
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;			
KW	chromosome identification; chromosome mapping; gene mapping;			
KW	gene therapy; cytostatic.			
XX	Homo sapiens.			
OS				
XX	WO2004030615-A2.			
FN	15-APR-2004.			
XX	29-SEP-2003; 2003WO-US028547.			
XX	02-OCT-2002; 2002US-041971P.			
PR	(GETH) GENENTECH INC.			
XX	Wu TD, Zhang Z, Zhou Y;			
XX	WPI; 2004-347921/32.			
DR	N-PSDB; ACN3937A.			
XX	New tumor-associated antigenic target polypeptides and nucleic acids,			
PT	useful in preparing a medicament for treating or detecting a			
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or			
PT	prostate cancer or tumor.			
XX	Claim 12; SEQ ID NO 3477; 7273pp; English.			
XX	The invention relates to human tumour-associated antigenic target (TAT)			
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are			
CC	overexpressed in cancer tissues compared to normal tissues, and may thus			
CC	serve as effective targets for the diagnosis and treatment of cancer in			
CC	mammals. The invention also relates to nucleic acid and polypeptide			
CC	sequences at least 80% identical to the TAT nucleic acids and			
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic			
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic			
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a			
CC	TAT polypeptide; and methods and compositions for the treatment or			
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,			
CC	antibodies, antagonists, binding molecules and compositions are useful			
CC	for diagnosing or treating a cell proliferative disorder associated with			
CC	increased TAT expression, particularly cancers such as breast cancer,			
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder			
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central			
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be			
CC	used as hybridisation probes, in chromosome and gene mapping, in			
CC	chromosome identification and in gene therapy. The present sequence			
CC	represents a TAT polypeptide of the invention			
XX	Sequence 435 AA;			
XX	Query Match 100.0%; Score 1133; DB 8; Length 435;			
XX	Best Local Similarity 100.0%; Pred. No. 2.8e-78;			
XX	Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	SQPAVPPVASENQTCRDEKEYYRPHQIRCCRCPPGTYYSAKCSIRDTVCATCAENS	60	
Db	28	SQPAVPPVASENQTCRDEKEYYRPHQIRCCRCPPGTYYSAKCSIRDTVCATCAENS	87	
Qy	61	YNEHNYLTICQLCRPCDPVWGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD	120	

SQ Sequence 439 AA;
Query Match 100.0%; Score 1133; DB 8; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.8e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPVASENQTCDQEKYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 60
DB 28 SQQAVPPVASENQTCDQEKYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 87

QY 61 YNEHWNLYTICQLCRPCDPVGMGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLYTICQLCRPCDPVGMGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPGTAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 13
ID ABM83610 standard; protein; 446 AA.
AC ABM83610;
XX
DT 18-NOV-2004 (first entry)
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3859.
XX
KW Gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Feralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42262.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 446 AA;
Query Match 100.0%; Score 1133; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.8e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPVASENQTCDQEKYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 60
DB 28 SQQAVPPVASENQTCDQEKYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 87

QY 61 YNEHWNLYTICQLCRPCDPVGMGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLYTICQLCRPCDPVGMGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPGTAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 14
ADJ67640
ID ADJ67640 standard; protein; 450 AA.
XX
AC ADJ67640;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human ovarian specific polypeptide SEQ ID NO:354.
XX
XX human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;
KW ovarian cancer; immune response; cancer.
XX
XX Homo sapiens.
XX
XX WO2004013311-A2.
XX
PD 12-FEB-2004.
XX
PF 06-AUG-2003; 2003WO-US024669.
XX
PR 06-AUG-2002; 2002US-0401469P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Salceda S, Liu C, Sun Y, Turner LR;
PI WPI; 2004-169331/16.
XX
XX New ovarian specific nucleic acid, useful in identifying, diagnosing,
PT monitoring, staging, imaging and treating ovarian cancer and non-
PT cancerous disease states in ovarian tissue.
XX
XX Claim 12; SEQ ID NO 354; 586pp; English.
XX
XX The invention relates to novel isolated ovarian specific nucleic acid
XX molecules and the polypeptides encoded by them. A protein of the
CC invention has cytostatic and immunostimulant activity. A nucleic acid
CC the invention may have a use as a vaccine, and in gene therapy. The

CC nucleic acid molecule or polypeptide, antibody or kit is useful in
CC identifying, diagnosing, monitoring, staging, imaging and treating
CC ovarian cancer and non cancerous disease states in ovarian tissue and in
CC inducing an immune response against the ovarian cancer cell. The
CC sequences shown in ADU67535-ADU67682 represent ovarian specific
CC polypeptides of the invention.

RESULT 15
ABP96136
ID ABP96136 standard; protein: 399 AA.

DT 09-MAY-2003 (first entry)

Human TNF receptor 2 related protein variant SEO ID NO:1.

Human; tumour necrosis factor receptor 2 related protein variant;
TNFR2pV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;;
TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
asthma; ulcerative colitis.

Homo sapiens.

PN WO2003012037-A2.

13-FEB-2003.

24-JUL-2002: 2002WO-US023684-

27-JUL-2001: 2001US-00917372.

PA (INCY-) INCYTE GENOMICS INC.

PI Lal PG, Warren BA:

WPI: 2003-256445/25.

XX
N-ESDB; ABZ/9/11/.

New cDNA, useful for preparing a composition for treating a disease or PT
PT condition associated with increased TNF signaling e.g., cancer of the PT
PT prostate, ovary, gallbladder, breast, brain, liver or colon, or PT
PT rheumatoid arthritis, asthma.

PS Claim 20; Fig 1A-F; 64pp; English.

The present sequence represents human tumour necrosis factor receptor 2 related protein variant (TNFR2pv). TNFR2pv has cytostatic, antiasthmatic and immunosuppressive activities, and can be used in gene therapy. The TNFR2pv cDNA or protein sequences can be used for preparing a composition

CC for treating a disease or condition associated with increased TNF
CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
CC arthritis, asthma or ulcerative colitis
XX
XX Sequence 199 AA.

Search completed: September 23, 2005, 10:27:33
Job time : 75 secs

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OM protein - protein search, using sw model

Run on: September 23, 2005, 09:52:51 ; Search time 43 Seconds
(without alignments)
341.997 Million cell updates/sec

Title: US-10-077-406-1
Perfect score: 1133
Sequence: 1 SQQAVPPYASENQTCRDOE.....QSDTTCKNPLEPLPEMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	197	2	US-08-505-606-1
2	1133	100.0	197	4	US-09-000-166-1
3	1133	100.0	197	4	US-09-303-262-1
4	1133	100.0	473	4	US-09-949-016-7944
5	987	87.1	170	4	US-08-828-683A-14
6	981	86.6	170	4	US-09-523-323-57
7	771	68.0	415	3	US-09-006-353A-6
8	771	68.0	415	4	US-09-573-986-6
9	456	40.2	77	3	US-08-866-545-3
10	456	40.2	77	3	US-09-627-775-3
11	305	26.9	227	3	US-08-974-022-48
12	305	26.9	227	3	US-08-795-445A-48
13	305	26.9	227	3	US-08-795-447A-48
14	305	26.9	227	3	US-08-974-186-48
15	305	26.9	227	3	US-08-795-446B-48
16	305	26.9	227	3	US-08-706-945D-134
17	305	26.9	227	4	US-08-577-788C-48
18	305	26.9	235	3	US-09-326-394-4
19	305	26.9	235	4	US-09-580-235-2
20	305	26.9	235	4	US-09-580-235-8
21	305	26.9	235	4	US-09-580-181-2
22	305	26.9	235	4	US-09-580-181-8
23	305	26.9	235	4	US-09-102-530-2
24	305	26.9	235	4	US-09-102-530-8
25	305	26.9	237	4	US-09-579-845-10
26	305	26.9	461	1	US-08-385-229-2
27	305	26.9	461	2	US-08-650-000-2

28	305	26.9	461	3	US-09-042-785A-7	Sequence 7, Appli
29	305	26.9	461	3	US-08-477-347-3	Sequence 3, Appli
30	305	26.9	461	3	US-09-006-353A-4	Sequence 4, Appli
31	305	26.9	461	3	US-08-476-862-2	Sequence 2, Appli
32	305	26.9	461	4	US-09-573-986-4	Sequence 4, Appli
33	305	26.9	461	4	US-08-406-824A-2	Sequence 2, Appli
34	305	26.9	461	4	US-09-800-909-2	Sequence 2, Appli
35	305	26.9	461	4	US-09-758-124-2	Sequence 2, Appli
36	305	26.9	461	4	US-09-800-908-3	Sequence 3, Appli
37	305	26.9	461	4	US-09-896-096A-17	Sequence 17, Appli
38	305	26.9	461	4	US-09-949-016-6019	Sequence 6019, Ap
39	305	26.9	461	6	5395760-2	Patent No. 5395760
40	305	26.9	461	6	5395760-2	Patent No. 5395760
41	305	26.9	486	1	US-08-243-010-1	Sequence 1, Appli
42	305	26.9	491	4	US-09-949-016-7840	Sequence 7840, Ap
43	305	26.9	518	1	US-08-385-229-4	Sequence 4, Appli
44	305	26.9	518	4	US-09-579-845-1	Sequence 1, Appli
45	305	26.9	518	4	US-09-579-845-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-505-606-1
; Sequence 1, Application US/08505606
; Patent No. 5925351
; GENERAL INFORMATION:
; APPLICANT: BROWNING, Jeffrey L.
; APPLICANT: BENJAMIN, Christopher D.
; APPLICANT: HOCHMAN, Paula S.
; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
; TITLE OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS
; TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,606
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378,968
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, Jr., James F.
; REGISTRATION NUMBER: 27,794
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELETYPE: 14-8367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-505-606-1

Query Match 100.0%; Score 1133; DB 2; Length 197;

SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-828-683A-14

Query Match 87.1%; Score 987; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-85;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TCRDQKEYYEPQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENSYNEHWNLYTICQLC 74
Db 1 TCRDQKEYYEPQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENSYNEHWNLYTICQLC 60

QY 75 RCPDQVPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPGTEAELEKDEVG 134
Db 61 RCPDQVPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPGTEAELEKDEVG 120

QY 135 KGNHCVCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSDTTCK 184
Db 121 KGNHCVCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSDTTCK 170

RESULT 6
US-09-523-323-57
Sequence 57, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000C
CURRENT APPLICATION NUMBER: US/09/523,323
EARLIER FILING DATE: 2000-03-10
EARLIER FILING DATE: 1999-12-02
EARLIER FILING DATE: 1999-08-11
EARLIER FILING DATE: 1999-07-06
EARLIER FILING DATE: 1999-06-04
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-02-19
EARLIER FILING DATE: 1998-02-20
EARLIER FILING DATE: 1998-02-20
EARLIER FILING DATE: 1998-02-20
EARLIER FILING DATE: 1998-01-07
EARLIER FILING DATE: 1997-03-21
EARLIER FILING DATE: 1996-03-22
EARLIER FILING DATE: 1996-03-22
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: (7)
OTHER INFORMATION: May be any amino acid
US-09-523-323-57

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 7944
LENGTH: 473
TYPE: PRT
ORGANISM: Human
US-09-949-016-7944

Query Match 100.0%; Score 1133; DB 4; Length 473;
Best Local Similarity 100.0%; Pred. No. 9e-99; 0; Indels 0; Gaps 0;
Matches 197; Conservative 0; Mismatches 0;

QY 1 SQPQAVPPYASENOTCRDQKEYYEPQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENS 60
Db 66 SQPQAVPPYASENOTCRDQKEYYEPQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENS 125

QY 61 YNEHWNLYTICQLCRPCDPVPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
Db 126 YNEHWNLYTICQLCRPCDPVPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 185

QY 121 CPDQTEAELEKDEVGKGNHCVCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 180
Db 186 CPDQTEAELEKDEVGKGNHCVCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 245

QY 181 TTCKNPLEPLPPMSGT 197
Db 246 TTCKNPLEPLPPMSGT 262

RESULT 5
US-08-828-683A-14
Sequence 14, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:

	Query Match	86.6%	Score 981;	DB 4;	Length 170;
	Best Local Similarity	99.4%;	Pred. No. 6e-85;		
	Matches 169;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	15	TCRDEKEYVYPOHRI	CCSRCPGTYYS	AKCSIRDTVCATCA	NSYNEHNYLTICQLC 74
DB	1	TCRDEXEYVYPOHRI	CCSRCPGTYYS	AKCSIRDTVCATCA	NSYNEHNYLTICQLC 60
QY	75	RPCDPVMGLEIA	PCTSKRKTQCR	QCGMFCAAWALECTHCELLSDCPGTEAEELKDEVG 134	
DB	61	RPCDPVMGLEIA	PCTSKRKTQCR	QCGMFCAAWALECTHCELLSDCPGTEAEELKDEVG 120	
QY	135	KGNHNCVCKAGH	QNTSSPSAR	CQPHTRCENOG	LVAAAPGTAQSDTTCK 184
DB	121	KGNHNCVCKAGH	QNTSSPSAR	CQPHTRCENOG	LVAAAPGTAQSDTTCK 70

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,545
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009113-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265535e
; US-08-866-545-3

Query Match 40.2%; Score 456; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 7e-36; 0; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 0;

; QY 52 VCATCAENSYNEHWNLYTICQLCRPCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE 111
; Db 1 VCATCAENSYNEHWNLYTICQLCRPCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE 60

; QY 112 CTHCELLSDCPPGTEAE 128
; Db 61 CTHCELLSDCPPGTEAE 77

RESULT 10
US-09-627-775-3
; Sequence 3, Application US/09627775
; Patent No. 6682739
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark
; APPLICANT: Murali, Ramachandran
; APPLICANT: Aoki, Kazuhiko
; APPLICANT: Baron, Roland
; TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
; FILE REFERENCE: UPN3832
; CURRENT APPLICATION NUMBER: US/09/627,775
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,090
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-627-775-3

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 7e-36; 0; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 0;

; QY 52 VCATCAENSYNEHWNLYTICQLCRPCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE 111
; Db 1 VCATCAENSYNEHWNLYTICQLCRPCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE 60

; QY 112 CTHCELLSDCPPGTEAE 128
; Db 112 CTHCELLSDCPPGTEAE 128
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Db 61 CTHCELLSDCPPGTEAE 77

RESULT 11
US-08-974-022-48
; Sequence 48, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 3.9e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

; QY 5 AVPPYASE-NOTCRDQEKEYEPQHRICCSRCPCPGTYVSAGKSRIKDTVCATCAENSYNE 63
; Db 28 APTPYAPPGSTCR--LREYVDQTAQMCCKSCSPQHAKVFCTKTSDTVCDCSDSTYIQ 85
; QY 64 HNNYLTICQLCR---PCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE--CTHCELLS 119
; Db 86 LNNVPECLSCGSRCSQV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
; QY 120 DCPPG-----TEALKDEVGKNNHCVPCKAGHFONTSSPSARCOPHTRCENQGLVEAP 174
; Db 142 KCRPGFGVARPGTETSDVW-----CKPCAPGTFNTTSSDTICPHQICN-----VVAIP 191
; QY 175 GTAQSDTTC--KNPLEPLPP 192
; Db 192 GNASRDVACTSTSPTRSNAP 211

RESULT 12
US-08-795-445A-48
; Sequence 48, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
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ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 3.9e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NOTCRDQEKYEYEPQHRICCSRCPPGTYVSNAKSRIRDTCATCAENSYN 63
Db 28 AFTPYAPEPGSTCR--LREYDQTAQMCCSKSPGQHAKVFCCTKTSDTVCDSCEDSTYTQ 85
QY 64 HNNYLITICOLCR---PCDPVMGLEELIAPCTSKRKTCRCQCPGMFCAAWALE-CTHCELLS 119
Db 86 LNNWVPECLSCGSRCSDDV-----EQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
QY 120 DCPPG-----TEAEKDEYKGNHNCVPCKAGHFONTSSPSARCOPHTRCENQGLVEAAP 174
Db 142 KCRPGFGVARPGTETSDVV-----CKPCAPGTFTSNTSSTDICRPHQICN----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVAVCTSTSPTRSMAP 211

RESULT 15

US-08-795-446B-48
Sequence 48, Application US/08795446B
Patent No. 6288032
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-795-446B-48
Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 3.9e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NOTCRDQEKYEYEPQHRICCSRCPPGTYVSNAKSRIRDTCATCAENSYN 63
Db 28 AFTPYAPEPGSTCR--LREYDQTAQMCCSKSPGQHAKVFCCTKTSDTVCDSCEDSTYTQ 85
QY 64 HNNYLITICOLCR---PCDPVMGLEELIAPCTSKRKTCRCQCPGMFCAAWALE-CTHCELLS 119
Db 86 LNNWVPECLSCGSRCSDDV-----EQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
QY 120 DCPPG-----TEAEKDEYKGNHNCVPCKAGHFONTSSPSARCOPHTRCENQGLVEAAP 174
Db 142 KCRPGFGVARPGTETSDVV-----CKPCAPGTFTSNTSSTDICRPHQICN----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVAVCTSTSPTRSMAP 211

Search completed: September 23, 2005, 10:32:08
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2005, 10:26:27 ; Search time 64 Seconds
(without alignments)
1252.834 Million cell updates/sec

Title: US-10-077-406-1

Perfect score: 1133
Sequence: 1 SQPQAVPYASENQCRCDOE.....QSDTTCKNPLEPPMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues
Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Publicly Available Sequences
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	1133	100.0	197 13 US-10-003-211-1	Sequence 1, Appli
2	1133	100.0	197 17 US-10-077-406-1	Sequence 1, Appli
3	1133	100.0	435 9 US-09-907-372-19	Sequence 19, Appli
4	1133	100.0	435 9 US-09-907-372-19	Sequence 19, Appli
5	1133	100.0	435 10 US-09-917-372-19	Sequence 19, Appli
6	1133	100.0	435 13 US-10-087-192-942	Sequence 942, App
7	1133	100.0	435 14 US-10-087-192-942	Sequence 942, App
8	1133	100.0	435 15 US-10-291-480-6	Sequence 6, Appli
9	1133	100.0	435 15 US-10-369-300-17	Sequence 17, Appli
10	1133	100.0	435 15 US-10-262-445-133	Sequence 133, App
11	1129	99.6	399 9 US-09-907-372-1	Sequence 1, Appli
	1129	99.6	399 10 US-09-917-372-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-003-211-1
; Sequence 1, Application US/10003211
; Publication No. US20020197254A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and
; TITLE OF INVENTION: Anti-Lymphotoxin Receptor and Ligand Antibodies as
; TITLE OF INVENTION: Therapeutic Agents for the Treatment of Immunological
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: A013US
; CURRENT APPLICATION NUMBER: US/10/003,211
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: PCT/US97/19436
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/029,060
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-003-211-1

Query Match 100.0%; Score 1133; DB 13; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQPQAVPYASENQCRCDOEKEYEYFQHRICCSRCPPGTYYSAKCSRIKDTVCATCAENS 60
DB 1 SQPQAVPYASENQCRCDOEKEYEYFQHRICCSRCPPGTYYSAKCSRIKDTVCATCAENS 60

Qy	61	YNEHNYLTI	COL	CRPCDP	PWGLB	EAICT	SKRTK	QCRQ	CPGMP	CAAWALEC	THCELLSD	120
Db	61	YNEHNYLTI	COL	CRPCDP	PWGLB	EAICT	SKRTK	QCRQ	CPGMP	CAAWALEC	THCELLSD	120
Qy	121	CPPTGTEA	ELKDB	VGKGNH	CVPC	KAGH	QFNTSS	SPSAR	CQPHTR	CENQGL	VEAAPG	TAQSD 180
Db	121	CPPTGTEA	ELKDB	VGKGNH	CVPC	KAGH	QFNTSS	SPSAR	CQPHTR	CENQGL	VEAAPG	TAQSD 180

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RESULT 2
US-10-077-406-1
; Sequence 1, Application US/10077406
; Publication No. US20050037003A1
; GENERAL INFORMATION:
; APPLICANT: Browning, et al.
; TITLE OF INVENTION: Soluble Lymphotoxin-B Receptors and Anti-lymphotoxin
; TITLE OF INVENTION: Receptor and Ligand Antibodies, as Therapeutic Agents
; TITLE OF INVENTION: for the Treatment of Immunological Disease.
; FILE REFERENCE: B191
; CURRENT APPLICATION NUMBER: US/10/077,406
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US/09/000,166
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/US96/12010
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-406-1

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RESULT 3
US-09-907-372-19
; Sequence 19, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 435

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? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? OTHER INFORMATION: Incyte ID No. US20020068242A1 g339762
US-09-907-372-19

Query Match 100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0;

Qy 1 SQPAVPVYASENQTCRDQEKYVYEPQHRICCSRCPPGTIVYSAKSCSRIDTV
Db 28 SQPAVPVYASENQTCRDQEKYVYEPQHRICCSRCPPGTIVYSAKSCSRIDTV
Qy 61 YNEHWNLYITIQLCRPCDPVVMGLEBIAPCTSKRKTQCRQCPGMFCAAWALEC
Db 88 YNEHWNLYITIQLCRPCDPVVMGLEBIAPCTSKRKTQCRQCPGMFCAAWALEC
Qy 121 CPPGTAEALKDEVGKGNHCVPCKAGHFONTSSPSARCOPHTCENOGLEVA
Db 148 CPPGTAEALKDEVGKGNHCVPCKAGHFONTSSPSARCOPHTCENOGLEVA
Qy 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 4
US-09-768-779A-6
? Sequence 6, Application US/09768779A
? Patent No. US20020127637A1
? GENERAL INFORMATION:
? APPLICANT: NI, JIAN
? MOORE, PAUL
? TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
? RECEPTOR-LIKE PROTEIN 8
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: HUMAN GENOME SCIENCES, INC.
? STREET: 9410 KEY WEST AVENUE
? CITY: ROCKVILLE
? STATE: MD
? COUNTRY: US
? ZIP: 20850
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/768,779A
? FILING DATE: 25-Jan-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/086,582
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: KENLEY K. HOOVER
? REGISTRATION NUMBER: 40,302
? REFERENCE/DOCKET NUMBER: PF368PP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (301) 309-8504
? TELEFAX: (301) 309-8439
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 435 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-768-779A-6

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Query Match      100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 60
DB 28 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVWGLEELIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLTICQLCRPCDPVWGLEELIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 5
US-09-917-372-19
; Sequence 19, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030068619A1 g339762
US-09-917-372-19
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Query Match      100.0%; Score 1133; DB 10; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 60
DB 28 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVWGLEELIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLTICQLCRPCDPVWGLEELIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224
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RESULT 6
US-10-087-192-942
; Sequence 942, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
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```
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 942
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-942

Query Match      100.0%; Score 1133; DB 13; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 60
DB 28 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVWGLEELIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLTICQLCRPCDPVWGLEELIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224
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RESULT 7
US-10-291-480-6
; Sequence 6, Application US/10291480
; Publication No. US2003010069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: PF368CD1
; CURRENT APPLICATION NUMBER: US/10/291,480
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/768,779
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/086,582
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/048,020
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 435
; TYPE: PRT
; ORGANISM: human
US-10-291-480-6
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Query Match      100.0%; Score 1133; DB 14; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 60
DB 28 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVWGLEELIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNLTICQLCRPCDPVWGLEELIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 147
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QY 121 CPPGTEAELKDEYVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEYVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 8
US-10-369-300-17
; Sequence 17, Application US/10369300
; Publication No. US20030215442A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher
; APPLICANT: Hancock, Wayne
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
; TITLE OF INVENTION: IMMUNE DISORDERS USING COMBINATION THERAPY
; FILE REFERENCE: 7853-255
; CURRENT APPLICATION NUMBER: US/10/369,300
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,463
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-300-17

Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTYVSACSRIRDTVTCATCAENS 60
Db 28 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTYVSACSRIRDTVTCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVMGLEEIAPTCKSKRTQCRQCPGMFCAAWALECTHCELLSD 120
Db 88 YNEHWNLYTICQLCRPCDPVMGLEEIAPTCKSKRTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAELKDEYVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEYVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 9
US-10-262-445-133
; Sequence 133, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
```

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; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 133
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-445-133

Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTYVSACSRIRDTVTCATCAENS 60
Db 28 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTYVSACSRIRDTVTCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVMGLEEIAPTCKSKRTQCRQCPGMFCAAWALECTHCELLSD 120
Db 88 YNEHWNLYTICQLCRPCDPVMGLEEIAPTCKSKRTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAELKDEYVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEYVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 10
US-09-907-372-1
; Sequence 1, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
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Db 194 PLEPLPPMSGT 205

RESULT 13

US-10-112-793-14
; Sequence 14, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-112-793-14

Query Match 87.1%; Score 987; DB 13; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.8e-74; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0;

QY 15 TCRDQKEYEYPOHRIICCSRCPPGTYSKCSIRDTVCATCAENSYNEHWNLYTICQLC 74
Db 1 TCRDQKEYEYPOHRIICCSRCPPGTYSKCSIRDTVCATCAENSYNEHWNLYTICQLC 60
QY 75 RCPDVPVWGLEEIAPTCKSKRTQCRCPGMFCAAWALECTHCELLSDCPPGTEAEKDEVG 134
Db 61 RCPDVPVWGLEEIAPTCKSKRTQCRCPGMFCAAWALECTHCELLSDCPPGTEAEKDEVG 120
QY 135 KGNHNCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 184
Db 121 KGNHNCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 170

RESULT 14

US-10-375-680-57
; Sequence 57, Application US/10375680
; Publication No. US20040009147A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ruben, Steven M
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000E
; CURRENT APPLICATION NUMBER: US/10/375,680
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,234
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)-(7)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-375-680-57

Query Match 85.6%; Score 970; DB 15; Length 172;
Best Local Similarity 98.3%; Pred. No. 1e-72; Indels 2; Gaps 1;
Matches 169; Conservative 0; Mismatches 1;
QY 15 TCRDQEE--KEYEYPOHRIICCSRCPPGTYSKCSIRDTVCATCAENSYNEHWNLYTICQ 72
Db 1 TCRDQEAAYEYPOHRIICCSRCPPGTYSKCSIRDTVCATCAENSYNEHWNLYTICQ 60
QY 73 LCRPCDPVWGLEEIAPTCKSKRTQCRCPGMFCAAWALECTHCELLSDCPPGTEAEKDE 132
Db 61 LCRPCDPVWGLEEIAPTCKSKRTQCRCPGMFCAAWALECTHCELLSDCPPGTEAEKDE 120
QY 133 VGKGNHNCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 184
Db 121 VGKGNHNCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 172

RESULT 15

US-09-948-018-19
; Sequence 19, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-948-018-19

Query Match 68.8%; Score 780; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.7e-57; Indels 0; Gaps 0;
Matches 135; Conservative 0; Mismatches 0;
QY 63 EHWNYLTICQLCRPCDPVWGLEEIAPTCKSKRTQCRCPGMFCAAWALECTHCELLSDCP 122
Db 1 EHWNYLTICQLCRPCDPVWGLEEIAPTCKSKRTQCRCPGMFCAAWALECTHCELLSDCP 60
QY 123 PGTEAEKDEYKGNHNCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 182
Db 61 PGTEAEKDEYKGNHNCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 120

QY 183 CKNPLEPLPPMSGT 197
Db 121 CKNPLEPLPPMSGT 135

Search completed: September 23, 2005, 10:33:18
Job time : 66 secs

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OM protein - protein search, using sw model

Run on: September 23, 2005, 09:46:31 ; Search time 40 Seconds
(without alignments)
473.868 Million cell updates/sec

Title: US-10-077-406-1

Perfect score: 1133

Sequence: 1 SQPQAVPPYASENQTCDQEQE.....QSDYTKNPLPLPPMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	435	2 I54182	tumor necrosis fac
2	305	26.9	461	1 A35356	tumor necrosis fac
3	295	26.0	474	2 B38634	tumor necrosis fac
4	290	25.6	459	2 I48854	gene murine tumour
5	278	24.5	277	2 A60771	B-cell activation
6	243.5	21.5	305	2 A46476	B cell-associated
7	226.5	20.0	651	2 JC7705	death receptor-6 -
8	222.5	19.6	271	2 S12783	OX40 antigen precu
9	214.5	18.9	272	2 I48700	gene ox40 protein
10	210.5	18.6	455	1 GQUT1	tumor necrosis fac
11	210	18.5	348	2 T28623	hypothetical prote
12	210	18.5	349	2 B36858	gene G4R protein -
13	207	18.3	349	2 D72175	G2R protein - vari
14	206	18.2	461	2 JC4302	tumor necrosis fac
15	201	17.7	277	2 I37552	OX40 homolog - hum
16	201	17.7	454	1 GQMT1	tumor necrosis fac
17	196	17.3	595	2 A42086	CD30 antigen precu
18	195.5	17.3	255	2 I38426	lymphocyte activat
19	189	16.7	325	2 B43692	T2 protein - rabbi
20	187.5	16.5	314	2 I37383	PAS soluble protei
21	184.5	16.3	461	1 GQUT1	tumor necrosis fac
22	183.5	16.2	326	1 GQVZML	T2 protein - myxom
23	181	16.0	335	2 A40036	apoptosis-mediati
24	179.5	15.8	256	2 B32393	T-cell antigen 4-1
25	171.5	15.1	425	1 A26431	nerve growth facto
26	166	14.7	493	2 JC5486	membrane glycoprot
27	164	14.5	416	1 JN0006	nerve growth facto
28	162	14.3	327	2 A46484	apoptosis-mediati
29	148.5	13.1	427	1 GQHUN	nerve growth facto

ALIGNMENTS

RESULT 1

I54182

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C:Accession: I54182

R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993.

A:Title:--Construction-and-evaluation of a hncDNA library of human l2p transcribed sequ

A:Reference number: I54182; MUID:93252381; PMID:8486360

A:Accession: I54182

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-435 <RES>

A:Cross-references: UNIPROT:P36941; GB:I04270; NID:g339761; PIDN:AAA36757.1; PID:g33976

C:Genetics:

A:Gene: GDB:LTBR

A:Cross-references: GDB:1230195; OMIM:600979

A:Map position: l2p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homol

Query Match	100.0%	Score 1133;	DB 2;	Length 435;
Best Local Similarity	100.0%;	Pred. No. 5.8e-78;		
Matches 197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SQPQAVPPYASENQTCDQEQEYYPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS	60	
DB	28	SQPQAVPPYASENQTCDQEQEYYPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS	87	
QY	61	YNEHWNLYTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCLLS	120	
DB	88	YNEHWNLYTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCLLS	147	
QY	121	CPFGTEAEALKDVGKNNHCVPCKAGHFQNTSSPASCQPHTRCENQGLVEAAGTQASD	180	
DB	148	CPFGTEAEALKDVGKNNHCVPCKAGHFQNTSSPASCQPHTRCENQGLVEAAGTQASD	207	
QY	181	TTCKNPLPLPPMSGT 197		
DB	208	TTCKNPLPLPPMSGT 224		

RESULT 2

A35356

tumor necrosis factor receptor 2 precursor [validated] - human

N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094

R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.

Science 248, 1019-1023, 1990

A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

Db 90 QPFTCLSCSSCTDQV-----ETRACTKQONRVCAACEAGRYCALKTHSGSCRCQWLSKC 145

QY 122 PGTEAELEKDEVGKGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQSDT 181

Db 146 GGF-GVASSRPNNGVLKACAPGTFTSDTSDVCRPHRCS-----ILAIPGNASTDA 200

QY 182 TCKNPLEPLPPMS 195

Db 201 VC-----APESPTLS 210

RESULT 4

I48854

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48854

Mamm. Genome 5, 726-727, 1994

A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A:Reference number: I48854; MUID:95178848; PMID:7873884

A:Accession: I48854

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-459 <RES>

A:Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:q43380; PIDN:CAA53981.1; PID:q4338

C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog

F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 25.6%; Score 290; DB 2; Length 459;

Best Local Similarity 33.5%; Pred. No. 1e-14;

Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASE-NQTCRQDEKEYEYEPQHRICCSRCPPTGYTVSAKSRIRDTVCATCAENSYNEHWN 66

Db 16 PYKPEPGYECQISQ-EYDRKAQMCCKAPGQGVYKHFNCNKTSDTVCADCEASMTQVWN 74

QY 67 YLTICQLCR---PCDPVMGLEBIAPCTSKRKTQCRQCPGMFCA--AWALECTHCELLSDC 121

Db 75 QPFTCLSCSSCTDQV-----ETRACTKQONRVCAACEAGRYCALKTHSGSCRCQWLSKC 130

QY 122 PGTEAELEKDEVGKGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQSDT 181

Db 131 GGF-GVASSRPNNGVLKACAPGTFTSDTSDVCRPHRCS-----ILAIPGNASTDA 185

QY 182 TCKNPLEPLPPMS 195

Db 186 VC-----APESPTLS 195

RESULT 5

A60771

B-cell activation protein CD40 precursor - human

N:Alternate names: B-cell surface antigen Bp50

C:Species: Homo sapiens (man)

C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: S04460; A60771

R:Stamenkovic, I.; Clark, E.A.; Seed, B.

EMBO J. 8, 1403-1410, 1989

A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor

A:Reference number: S04460; MUID:89356608; PMID:2475341

A:Accession: S04460

A:Molecule type: mRNA

A:Residues: 1-277 <STA>

A:Cross-references: UNIPROT:P25942; EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851

R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.

J. Immunol. 142, 562-567, 1989

A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like

A:Reference number: A60771; MUID:89093941; PMID:2463309

A:Accession: A60771

A:Molecule type: protein

A:Residues: 21-50 <BRA>

A:Experimental source: Burkitt lymphoma cell line Raji

C:Genetics:

A:Gene: GDB:CD40

A:Cross-references: GDB:215268; OMIM:109535

A:Map position: 20q12-20q13.2

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein.

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-193/Domain: B-cell activation protein CD40 #status experimental <MAT>

F:21-193/Domain: extracellular #status predicted <EXT>

F:194-215/Domain: transmembrane #status predicted <TM>

F:216-277/Domain: intracellular #status predicted <CYT>

F:153,180/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 24.5%; Score 278; DB 2; Length 277;

Best Local Similarity 35.0%; Pred. No. 5.5e-14;

Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PPYASENQTCRQDEKEYEYEPQHRICCSRCPPTGYTVSAKSRIRDTVCATCAENSYNEHWN 66

Db 22 PPTA-----CR--EKYLLNSQ--CCSLCQPGQKLVSDCTETETECCLPGSESEFLDTWN 72

QY 67 YLTICQLCRPCDPVMGLEBIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPCPTE 126

Db 73 RETHCHQHKYCDPNLGLRVQKGTSETDTICTCEBGMHCTSEA--CESCVLHRSCTSPGFG 130

QY 127 AELKDEVGKGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQSDTTC 183

Db 131 VK-QIATGVSDTICPCPVGPFPSNVSSAFKCHPMTSCETKOLVQQAGTKNTKDVVC 186

RESULT 6

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A46476; A46515

R:Torres, R.M.; Clark, E.A.

J. Immunol. 148, 620-626, 1992

A:Title: Differential increase of an alternatively polyadenylated mRNA species of murin.

A:Reference number: A46476; MUID:92105763; PMID:1370315

A:Accession: A46476

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305 <TOR>

A:Cross-references: UNIPROT:P27512; GB:M83312; NID:g1553058

A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)

A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0

R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.

J. Immunol. 149, 3921-3926, 1992

A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A:Reference number: A46515; MUID:93094586; PMID:1281194

A:Accession: A46515

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-287, 'LV', <GRI>

A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; J.

A:Experimental source: BALB/c, liver

A:Note: sequence extracted from NCBI backbone (NCBI:P:120357)

C:Comment: For an alternative splice form, see PIR:A46515.

C:Comment: For an alternative splice form, see PIR:A46476.

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: alternative splicing; transmembrane protein

F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 21.5%; Score 243.5; DB 2; Length 305;

Best Local Similarity 31.0%; Pred. No. 2.3e-11;

Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;

QY 15 TCRDQKEYEYEPQHRICCSRCPPTGYTVSAKSRIRDTVCATCAENSYNEHWNVLTICQLC 74

Db 25 TCSD--KOYLHDGQ--CCDLCPQSGRLTSHCTALEKTCQCHPCDSGSEFSAQWNRIRCHQH 80

QY 75 RPCDPVWGLEELIAPCTSKRKTCRCQCPGMFCAAWALECTHCELLSDCPG-----TEAEL 129
Db 81 RHCEPNQGLRVKKEGAESDVTCTCKEGQHCT--SKDCEACAQHTPCIPFGFMEMATET 138
QY 130 KDEVGKGNHCVCKPCAGHCFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
Db 139 TDTV-----CHPCPVGFFSNQSSUPEKCYPTWTSCEDKNLEVLQKGTSTQNVIC 186

RESULT 7
JC7705
death receptor-6 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
C:Accession: JC7705
R:Briggham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A:Reference number: JC7705; MUID:21308433; PMID:11414698
A:Accession: JC7705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
A:Cross-references: UNIPROT:Q98SM6; GB:AF349908
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily, a cell death and/or survival signaling cascade.
C:Genetics:
A:Gene: dr-6
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homologous to TNFR1
C:Keywords: death receptor; TNF receptor; TNF receptor repeat homologous to TNFR1
F:1-21/Domain: signal sequence #status predicted <SIG>
F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F:332-350/Domain: transmembrane #status predicted <TM>
F:410-475/Domain: death domain #status predicted <DED>
F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 20.0%; Score 226.5; DB 2; Length 651;
Best Local Similarity 28.8%; Pred. No. 7.8e-10;
Matches 49; Conservative 26; Mismatches 62; Indels 33; Gaps 6;

QY 30 ICSCRCPPTGYYSVAKSRRDTRVTCATCAENSNEHWNLYITICOLCR-PCDPVWGLEELIAP 88
Db 50 LIIDKCPAGTYVSKHCTKTLRECSPCPDGTGTHKENGIERCHPCRKPC--LPMIEKTH 107
QY 89 CTSKRKTQCRQCPGWF-----CAAWALECTHCELLSDCP-----PGTEALKDEVGKG 136
Db 108 CTALTDRECTCLSGTFQINDTCVPTV-----CPVGVGRKKGTET----- 149
QY 137 NNHCVPCKAGHCFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCNKP 186
Db 150 DVMCKPCLRGTFSDVPSSVMKCKTYDCFGKQMVVVKPTKESDNVCKSP 199

RESULT 8
S12783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S12783; S08036
R:Mallett, S.; Fosseum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A:Reference number: S12783; MUID:90214614; PMID:2157591
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: UNIPROT:P15725; EMBL:X17037; NID:G57830; PIDN:CAA34897.1; PID:G57831
C:Superfamily: CD27 antigen; NGF receptor repeat homologous to TNFR1
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 19.6%; Score 222.5; DB 2; Length 271;
Best Local Similarity 32.1%; Pred. No. 7.8e-10;
Matches 53; Conservative 17; Mismatches 68; Indels 27; Gaps 5;

QY 21 KEYEPOHRIICSRCPPTGYYSVAKSRRDTRVTCATCAENSNEHWNLYITICOLCRPCDPV 80
Db 28 KDTYPSGHK-CCRECQPGHGMVSRCDHTRDITVCHPCPGFYNEAVNYDT-CKQCTQCNRH 85
QY 81 MGLEIAPCTSKRKTCRCQCPGMFCAAWALECTHCELLSDCPGTEALKDEVGKGNHC 140
Db 86 SGSELKQNCCTPTEDTVCRC-----PGTQPR-QDSSHKLGVDC 122
QY 141 VPCKAGHCFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCN 185
Db 123 VPCPGHFPSPGNSQA--CKPWTNCTLSGKIRHPASNSLDTVCED 165

RESULT 9
I48700
Gene ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhlmann, J.E.; van den Bortwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell interaction
A:Reference number: I48700; MUID:94044750; PMID:8228223
A:Accession: I48700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: UNIPROT:P47741; EMBL:Z21674; NID:G312827; PIDN:CAA79772.1; PID:G31288
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A:Reference number: I48334; MUID:95255413; PMID:7737295
A:Accession: I48334
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14,'G',16-272 <RES>
A:Cross-references: EMBL:X85214; NID:G732818; PIDN:CAA59476.1; PID:G732819
C:Genetics:
A:Gene: ox40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homologous to TNFR1

Query Match 18.9%; Score 214.5; DB 2; Length 272;
Best Local Similarity 31.7%; Pred. No. 3.1e-09;
Matches 53; Conservative 16; Mismatches 67; Indels 31; Gaps 6;

QY 21 KEYEPOHRIICSRCPPTGYYSVAKSRRDTRVTCATCAENSNEHWNLYITICOLCRPCDPV 80
Db 29 KHTYPSGHK-CCRECQPGHGMVSRCDHTRDITVCHPCPGFYNEAVNYDT-CKQCTQCNRH 86
QY 81 MGLEIAPCTSKRKTCRCQCPGMFCAAWALECTHCELLSDCPGTEALKDEVGKGNHC 140
Db 87 SGSELKQNCCTPTQDITVCRC-----PGTQPR-QDSGYKLGVDC 123
QY 141 VPCKAGHCFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCN 185
Db 124 VPCPGHFPSPGNSQA--CKPWTNCTLSGKIRHPASNSLDTVCED 166

RESULT 10
GQHTU1
tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
A:Reference number: A38208; A34899; A36555; A38281; S12057; JT0758; A60231; A38
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.

Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to chromosome 6p21
A:Reference number: A38208; MUID:92250049; PMID:131517
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: UNIPROT:P19438; GB:M75864; GB:M75865; GB:M75866; NID:G339748; PIDN:AA03210.1; PID:G339754
R:Oestercher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, C.; Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor (p55) cDNA
A:Reference number: A34899; MUID:90235284; PMID:2158862
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOE>
A:Cross-references: GB:M58286; GB:M33480; NID:G339753; PIDN:AAA36753.1; PID:G339754
A:Experimental source: placenta
A>Note: part of this sequence, including the amino end of the mature protein, confirmed by R. Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor- α
A:Reference number: A34900; MUID:90235285; PMID:2158863
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:G339745
R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor (p55) cDNA
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:G339755; PIDN:AAA36754.1; PID:G339756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 30-38; 41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104; 107-128; 162-167, 'X', 169-216
A>Note: the purified protein, called tumor necrosis factor binding protein, is a soluble protein of 216 kDa
R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.; Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant protein
A:Reference number: A38281; MUID:91017509; PMID:2170974
A:Accession: A38281
A:Molecule type: mRNA
A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
A>Note: the authors translated the codon TCG for residue 371 as Thr, AAG for residue 372 as Lys, and TGA for residue 373 as Stop
R:Nophar, Y.; Kemper, O.; Brakkebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, H.; EMBO J. 9, 3269-3278, 1990
A:Title: Soluble forms of tumor necrosis factor (TNF) receptors (TNF-Rs). The cDNA for the type I form of the receptor.
A:Reference number: S12057; MUID:91006021; PMID:1698610
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <NOP>
A:Cross-references: EMBL:X55313; NID:G37223; PIDN:CAA39021.1; PID:G37224
A>Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were cloned from a cDNA library
R:Kemper, O.; Wallach, D.; Gene 134, 209-216, 1993
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor receptor
A:Reference number: JT0758; MUID:94085779; PMID:8262379
A:Accession: JT0758
A:Molecule type: DNA
A:Residues: 1-13 <KEM>
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.; Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence, and characterization of an inhibitor (soluble tumor necrosis factor inhibitor)
A:Reference number: A60231; MUID:90292116; PMID:2113477
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, P.; Lucci III, J.A.; Jeffes, E.W.B.; Le Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor

tients.

A:Reference number: A38258; MUID:91062364; PMID:2174164

A:Accession: A38258

A:Molecule type: protein

A:Residues: 41-60 <GAT>

A:Experimental source: cancer patient serum

R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyrell, H.; Grubb, A.; Adolf, G.; Eur. J. Haematol. 42, 270-275, 1989

A:Title: Isolation and characterization of a tumor necrosis factor binding protein from human urine

A:Reference number: A60594; MUID:89171156; PMID:2924890

A:Accession: A60594

A:Molecule type: protein

A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XX', 60 <OLS>

A:Experimental source: renal failure patient urine

R:Engelmann, H.; Novick, D.; Wallach, D.; J. Biol. Chem. 265, 1531-1536, 1990

A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct binding sites

A:Reference number: A35010; MUID:9010215; PMID:2153136

A:Accession: A35010

A:Molecule type: protein

A:Residues: 41-45 <ENG>

A:Experimental source: normal urine

R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.; Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994

A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine

A:Reference number: JC2404; MUID:95128033; PMID:7765720

A:Accession: JC2404

A:Molecule type: protein

A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>

A:Experimental source: urine

C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin)

C:Genetics:

A:Gene: GDB:TNFR1

A:Cross-references: GDB:125913; OMIM:191190

A:Map position: 12p13.2-12p13.3

A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/3; 256/3; 353/1

A:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-21/Domain: signal sequence; status predicted <SIG>

F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>

F:30-201/Domain: extracellular #status predicted <EXT>

F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status predicted <INT>

F:44-82/Domain: NGF receptor repeat homology <NG1>

F:84-126/Domain: NGF receptor repeat homology <NG2>

F:127-167/Domain: NGF receptor repeat homology <NG3>

F:168-196/Domain: NGF receptor repeat homology <NG4>

F:212-234/Domain: transmembrane #status predicted <MEM>

F:235-455/Domain: intracellular #status predicted <INT>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.6%; Score 210.5; DB 1; Length 455;

Best Local Similarity 32.6%; Pred. No. 9.3e-09;

Matches 61; Conservative 19; Mismatches 84; Indels 23; Gaps 9;

QY 18 DOEK-----EYEPQHR-ICCSRCPPGTGVSAK-SRIRDTVCATCAENSYNEHMY 67

Db 36 DREKDSVCPQKYLHPNNSICCTCKHGTLYNDPCPGQDTCRECSGSFTASENH 95

QY 68 LTIQCLRPDPVGLIEIAPCTSKRTQCRQCPQMFCAWA---LECHTCLLSDCPPG 124

Db 96 LRAHCLSCSKCRKEMQVBISSCTVDRTVCGCRKQYRHYWSENLFQCFNCSL---CLNG 152

QY 125 TEAEALKDEVGKNNHCVCKAGHF--QNTSSPSARCPHTRCENQGL--VEAAPGTAQSD 180

Db 153 TVHLSQBE--KONTVCT-CHAGFFLRENEVCSCNCKSLECTKLCLOIENVKGTEDSG 209

QY 181 TTCKNPL 187

Db 210 TVVLLPL 216

RESULT 11

T28623

hypothetical protein G2R - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28623
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: UNIPROT:P34015; EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g4391
A:Experimental source: strain Bangladesh 1975
C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 18.5%; Score 210; DB 2; Length 348;
Best Local Similarity 29.0%; Pred. No. 8.3e-09;
Matches 45; Conservative 20; Mismatches 80; Indels 10; Gaps 5;

QY 8 PYASENQTRDOEKYEYFQHRICCSRCPPGTYVSAAKSRIRDVTCATCAENSYNHNY 67
DB 23 PYTPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSTNTQCTPCGSGTFTSRNNH 78
QY 68 LTICQLCR-PCDPVMGLEIAPCTSKRKTQCRQCPGMFC-AAWALECTHCELLSDCPPGT 125
DB 79 LPACLSNCRGN--SNQVETRSCNTHNRICEPSGYCLLKSGSGCKACVSQTKC--GI 134
QY 126 EAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCP 160
DB 135 GYGVSHTSVGDVICSPCGFGTYSHTVSSADKCEP 169

RESULT 12
D36858
Gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
A:Reference number: GenBank, November 1992
A:Accession: D36858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: UNIPROT:P34015; GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Froil
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A:Reference number: S46868
A:Accession: S46888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281; PMID:8384129
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics:
A:Gene: G4R
C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 18.5%; Score 210; DB 2; Length 349;
Best Local Similarity 29.0%; Pred. No. 8.3e-09;
Matches 45; Conservative 20; Mismatches 80; Indels 10; Gaps 5;

QY 8 PYASENQTRDOEKYEYFQHRICCSRCPPGTYVSAAKSRIRDVTCATCAENSYNHNY 67
DB 24 PYTPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSTNTQCTPCGSGTFTSRNNH 79
QY 68 LTICQLCR-PCDPVMGLEIAPCTSKRKTQCRQCPGMFC-AAWALECTHCELLSDCPPGT 125
DB 80 LPACLSNCRGN--SNQVETRSCNTHNRICEPSGYCLLKSGSGCKACVSQTKC--GI 135
QY 126 EAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCP 160
DB 136 GYGVSHTSVGDVICSPCGFGTYSHTVSSADKCEP 170

RESULT 13
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C:Accession: D72175
R:Shchelkunov, S.N.; Totnenin, A.V.; Gutorov, V.V.; Safronov, P.P.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: D72175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: UNIPROT:P34015; GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g583071
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: G2R
C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 18.3%; Score 207; DB 2; Length 349;
Best Local Similarity 29.0%; Pred. No. 1.4e-08;
Matches 45; Conservative 19; Mismatches 81; Indels 10; Gaps 5;

QY 8 PYASENQTRDOEKYEYFQHRICCSRCPPGTYVSAAKSRIRDVTCATCAENSYNHNY 67
DB 24 PYTPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSTNTQCTPCGSGTFTSRNNH 79
QY 68 LTICQLCR-PCDPVMGLEIAPCTSKRKTQCRQCPGMFC-AAWALECTHCELLSDCPPGT 125
DB 80 LPACLSNCRGN--SNQVETRSCNTHNRICEPSGYCLLKSGSGCKACVSQTKC--GI 135
QY 126 EAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCP 160
DB 136 GYGVSHTSVGDVICSPCGFGTYSVTSSTDKCEP 170

RESULT 14
JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A:Reference number: JC4302; MUID:96011645; PMID:7590278
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: UNIPROT:P50555; GB:U19994; NID:gl1141752; PIDN:AAC48499.1; PID:gl11417
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>

	Query Match	17.7%	Score 201;	DB 2;	Length 277;
	Best Local Similarity	28.3%;	Pred. No. 3.3e-08;		
	Matches	49;	Conservative	21;	Mismatches 73; Indels 30; Gaps 5;
Qy	26	PQHRICSRCPGGTYYSAKSGSRIDTVCATCAENSYNEHWNLYITICQLRCPDPPVWGLBEE	85		
Db	37	PSNDRCHECRPGNGWVSRCSQNTVCRPCGGFYNDVVSSKP-CKPCTWCLNRGSSR	95		
Qy	86	IAPDTCRKRKTQCRQCPGMFCAAWALBCTHCELLSDCPPGTEAELKDEVGKGNHCVCPCKA	145		
Db	96	KQLCTATQDTVCRCRAG-----TQPLDSYKPGVD-----CAPCP	130		
Qy	146	GHPQNTSSPSARCOPHTRCENOGIVEAAPCTAQSDTTC--KNPLEPLPPEMSG	196		
Db	131	GHPF--SPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRPDPATQPOETQG	181		

Search completed: September 23, 2005, 10:31:19
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2005, 09:44:31 ; Search time 175 Seconds
(without alignments)
576.455 Million cell updates/sec

Title: US-10-077-406-1

Perfect score: 1133

Sequence: 1 SQPQVPPYASENQTCRQDE.....QSDTTCKNPLEPPPMSET 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1133	100.0	435	1	TNR3 HUMAN	P36941 homo sapien
2	771	68.0	415	1	TNR3 MOUSE	P50284 mus musculus
3	309.5	27.3	483	1	Q800K7	Q800K7 paralicthby
4	305	26.9	461	1	TR1B HUMAN	P20333 h tumor nec
5	295.5	26.1	278	2	Q8SQ34	Q8SQ34 sus scrofa
6	295	26.0	474	1	TR1B MOUSE	P25119 mus musculus
7	291.5	25.7	433	2	Q91ZM6	Q91ZM6 rattus norv
8	291.5	25.7	461	2	Q6VAU8	Q6VAU8 rattus norv
9	291.5	25.7	474	1	TR1B RAT	Q62327 mus musculus
10	290	25.6	459	2	Q62327	Q62327 mus musculus
11	285.5	25.2	300	1	TR6B HUMAN	Q95407 homo sapien
12	284.5	25.1	274	2	Q7YRL5	Q7YRL5 canis famil
13	283	25.0	625	1	TR11 MOUSE	Q35305 mus musculus
14	278	24.5	223	2	Q86YK5	Q86YK5 homo sapien
15	278	24.5	277	1	TNR5 HUMAN	P25942 homo sapien
16	277	24.4	616	1	TR11 HUMAN	Q9Y6G6 homo sapien
17	266.5	23.5	387	2	Q6GLN3	Q6GLN3 xenopus lae
18	265.5	23.4	277	2	Q8WMQ2	Q8WMQ2 ovis aries
19	258	22.8	275	2	Q80WM9	Q80WM9 mus musculus
20	258	22.8	276	2	Q71F55	Q71F55 mus musculus
21	253	22.3	462	2	Q805B0	Q805B0 gallus gall
22	251.5	22.2	269	1	TNR5 BOVIN	Q28203 bos taurus
23	246.5	21.8	401	2	Q6P112	Q6P112 mus musculus
24	243.5	21.5	289	1	TNR5 MOUSE	P27512 mus musculus
25	243.5	21.5	289	2	Q8K2X6	Q8K2X6 mus musculus
26	242.5	21.4	283	2	Q9XSZ8	Q9XSZ8 cercopithec
27	242.5	21.4	401	1	T11B MOUSE	Q08712 mus musculus
28	240	21.2	186	2	Q72735	Q72735 cowpox viru
29	239.5	21.1	401	1	T11B HUMAN	Q00300 homo sapien
30	238.5	21.1	318	2	Q7T2H3	Q7T2H3 oncorhynch
31	238	21.0	302	2	Q9PUS0	Q9PUS0 salvelinus

32	235.5	20.8	401	1	T11B RAT	O08727 rattus norv
33	233.5	20.6	457	2	Q8IVS6	Q8IVS6 homo sapien
34	232.5	20.5	467	2	Q800I0	Q800I0 gallus gall
35	232	20.5	270	2	Q75SV8	Q75SV8 felis silve
36	230.5	20.3	283	1	TR14 HUMAN	Q92956 homo sapien
37	230	20.3	276	2	Q9DDD2	Q9DDD2 gallus gall
38	229.5	20.3	351	2	Q57117	Q57117 cowpox viru
39	229.5	20.3	285	2	Q90W71	Q90W71 oncorhynch
40	228.5	20.2	655	1	TR21 HUMAN	Q75509 homo sapien
41	226.5	20.0	167	2	Q8UYL3	Q8UYL3 vaccinia vi
42	226.5	20.0	655	1	TR21 MOUSE	Q9EPUS mus musculu
43	225.5	19.9	186	2	Q7ZZY5	Q7ZZY5 gallus gall
44	225.5	19.9	651	2	Q98SM6	Q98SM6 gallus gall
45	225	19.9	186	2	Q9YP87	Q9YP87 cowpox viru

ALIGNMENTS

RESULT 1
ID TNR3 HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE protein) (Tumor necrosis factor C receptor).
GN Name=LTBR; Synonyms=TNFRC, TNFRSF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12p
transcribed sequences derived from a somatic cell hybrid."
RL Genomics 16:214-218(1993);
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan K.J., Malek J.A., Guntar P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002)
[3]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor."
Science 264:707-710(1994).

```

RN RP CHARACTERIZATION.
RX MEDLINE=99223511; PubMed=10207006; DOI=10.1074/jbc.274.17.11868;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RL death in HeLa cells.";
RL J. Biol. Chem. 274:11868-11873(1999).
RN RP
RN RP FUNCTION.
RX MEDLINE=20261554; PubMed=10799510; DOI=10.1074/jbc.275.19.14307;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for LIGHT-
RT mediated apoptosis of tumor cells";
RL J. Biol. Chem. 275:14307-14315(2000).
RN RP
RN RP INTERACTION WITH TRAF3.
RX MEDLINE=96278943; PubMed=8663299; DOI=10.1074/jbc.271.25.14661;
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA Yagita H., Okumura K.;
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT the lymphotoxin-beta receptor.";
RL J. Biol. Chem. 271:14661-14664(1996).
RN RP
RN RP INTERACTION WITH TRAF4.
RX MEDLINE=98289299; PubMed=9626059;
RA Krajewski M., Krajewski S., Zapata J.M., VanArsdale T., Gascoyne R.D.,
RA Berern K., McFadden D., Shabalk A., Hugh J., Reynolds A.,
RA Clevenger C.V., Reed J.C.;
RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
RT adult, fetal, and tumor tissues.";
RL Am. J. Pathol. 152:1549-1561(1998).
RN RP
RN RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754; DOI=10.1016/S0378-1119(97)00616-1;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
RN RP
RN RP FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC
CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; L04270; AAA36757.1; -.
CC EMBL; BC026262; AAH26262.1; -.
CC F01; I54182; I54182.
CC HSP; Q92956; IJMA.
CC Genew; HGNC:6718; LTBR.
CC H-InvDB; HIX0010362; -.
CC MIM; 600979; -.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0004871; F:signal transducer activity; IEP.
CC GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. .; IEP.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR008063; Fas receptor.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00500; TNFR_NGFR_2; 3.

```

```

KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 435 Tumor necrosis factor receptor
FT TRANSMEM 228 247 Extracellular member 3.
FT DOMAIN 31 227 Potential.
FT TRANSMEM 228 247 Extracellular (Potential).
FT DOMAIN 249 435 Cytoplasmic (Potential).
FT REPEAT 42 81 TNFR-Cys 1.
FT REPEAT 82 124 TNFR-Cys 2.
FT REPEAT 125 168 TNFR-Cys 3.
FT REPEAT 169 211 TNFR-Cys 4.
FT DISULFID 43 52 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 80 By similarity.
FT DISULFID 83 98 By similarity.
FT DISULFID 101 116 By similarity.
FT DISULFID 104 124 By similarity.
FT DISULFID 126 132 By similarity.
FT DISULFID 139 148 By similarity.
FT DISULFID 142 167 By similarity.
FT DISULFID 170 185 By similarity.
FT CARBOHYD 40 40 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 100.0%; Score 1133; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 9.1e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCRDOEKEYEYEPQRIICSRCPGTYYSAKSRIKDTVCATCAENS 60
DB 28 SQQAVPPYASENQTCRDOEKEYEYEPQRIICSRCPGTYYSAKSRIKDTVCATCAENS 87
QY 61 YNEHWNYLTICQLCRPCDPVNMGLEEIAPTSKRTQCRQCPQMFCAAWALECTHCELLSD 120
DB 88 YNEHWNYLTICQLCRPCDPVNMGLEEIAPTSKRTQCRQCPQMFCAAWALECTHCELLSD 147
QY 121 CPPTGEALKEDEVGKNNHCVPCKAGHFQNTSSPSARCPQHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPTGEALKEDEVGKNNHCVPCKAGHFQNTSSPSARCPQHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 2
TNR3_MOUSE
ID TNR3_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (Lymphotoxin-beta receptor).
DE Name=Ltbr; Synonyms=TNFR, Tnfrsf3;
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S., Honjo T.;

```


TRIB_HUMAN STANDARD; PRT; 461 AA.
 ID P20333; Q16042; Q6Y129; Q9U1H1;
 AC 01-FEB-1991 (Rel. 17, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
 DE necrosis factor receptor 2) (TNF-R2) (tumor necrosis factor receptor
 DE type II) (p75) (p80 TNF-alpha receptor) (CD120b) (Btancerept)
 DE [Contains: Tumor necrosis factor binding protein 2 (TBPII) (TBP-2)].
 GN Name:TNFRSF1B; Synonyms:TNFR, TNFR2;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=90260639; PubMed=2160731;
 RX Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RT "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-196.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=96299745; PubMed=8661109; DOI=10.1006/geno.1996.0327;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 35:94-100(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND FUNCTION OF
 RP ISOFORM 2.
 RX PubMed=14688072; DOI=10.1093/intimm/dxh014;
 RA Lainez B., Fernandez-Real J.M., Romero X., Esplugues E., Canete J.D.,
 RA Ricart W., Engel P.;
 RT "Identification and characterization of a novel spliced variant that
 RT encodes human soluble tumor necrosis factor receptor 2.";
 RL Int. Immunol. 16:169-177(2004).
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANTS MET-187; ARG-196; LYS-232; THR-236;
 RP PRO-264 AND ARG-295.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND
 RP ARG-301.
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Kuldane K.S., Rajkumar N., Toth E.J., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattLESNPs. NHLBI HL6682 program for genomic applications, UW-
 RT FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=ENS;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 37-461 FROM N.A. (ISOFORM 1).
 RX MEDLINE=91370690; PubMed=1966549; DOI=10.1016/1043-4666(90)90022-L;
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
 RA Brockhaus M., Lesslauer W.;
 RT "Two human TNF receptors have similar extracellular, but distinct
 RT intracellular, domain sequences.";
 RL Cytokine 2:231-237(1990).
 RN [9]
 RP SEQUENCE OF 116-461 FROM N.A. (ISOFORM 1), PARTIAL SEQUENCE, AND
 RP VARIANT ARG-196.
 RX MEDLINE=90349572; PubMed=2166946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor and
 RT demonstration of a shed form of the receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 RN [10]
 RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
 RX MEDLINE=21069356; PubMed=11197692; DOI=10.1038/sj.gene.6363700;
 RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
 RT "New single nucleotide polymorphisms in the coding region of human
 RT TNFR2: association with systemic lupus erythematosus.";
 RL Genes Immun. 1:501-503(2000).
 RN [11]
 RP SEQUENCE OF 27-33.
 RC TISSUE=Urine;
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human urine.
 RT Evidence for immunological cross-reactivity with cell surface tumor
 RT necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [12]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RT "Purification and partial amino acid sequence analysis of two distinct
 RT tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [13]
 RP CHARACTERIZATION.
 RX MEDLINE=93016040; PubMed=1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [14]
 RP INTERACTION WITH TRAF2.
 RX MEDLINE=94349371; PubMed=8069916; DOI=10.1016/0092-8674(94)90532-0;
 RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
 RT "A novel family of putative signal transducers associated with the
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";

Db 192 GNASMDAVCTSTSPTRGMAP 211

RESULT 5

Q8SQ34 PRELIMINARY; PRT; 278 AA.

ID Q8SQ34 AC Q8SQ34

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CD40.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA West K.A., Li A.W., Rowden G.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.

RA EMBL; AF248545; AAL92924.1; .

DR HSP; P25942; 1FLL.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR008063; Fas receptor.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 1.

DR PRINTS; PR01680; FASRECEPTOR.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00500; TNFR_NGFR_2; 4.

SQ SEQUENCE 278 AA; 30551 MW; 20D446E44AP93DD2 CRC64;

Query Match 26.1%; Score 295.5; DB 2; Length 278;

Best Local Similarity 36.9%; Pred. No. 3.8e-17;

Matches 62; Conservative 19; Mismatches 74; Indels 13; Gaps 3

Qy 21 KEYEPQHRICSRCPGTVSACSRIRDTVCATCAENSYNEHWYLTICQLCPQDPV 80

Db 27 KENQYPTNSRCCNLCPPGQGLVNHCTEVTETELPCSSSEFLATNREKHKCHQHKYCDPN 86

Qy 81 MGLEIETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPPG-----TEAEIKDEVGK 135

Db 87 LGIQVQREGTSKDTTTCVCSGHHCTNSA--CRSCTLHSLCFPGGLGVQKQMATVSDTI-- 142

Qy 136 GNNHCYCPKAGHFQNTSSPSARCPQPTRCENQGLVEAAPGTAQSDTTTC 183

Db 143 ----CRPCPVGFFSNVSSASEKQPWTSCESKGLVEQRAGTKTKDVC 186

RESULT 6

TR1B_MOUSE

ID TR1B_MOUSE STANDARD; PRT; 474 AA.

AC P25119; O88734; P97893;

DT 01-MAY-1992 (Rel. 22, Created)

DT 25-JAN-2005 (Rel. 46, Last sequence update)

DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor

DE necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor

DE type II) (p75) (p80 TNF-alpha receptor).

GN Names=tnfrsf1b; Synonyms=tnfr-2, Tnfr2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91187885; Pubmed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H.,

RA Chen E.Y., Goeddel D.V.;

"Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;
 RA "Molecular cloning and expression of the type 1 and type 2 murine TNF receptors for tumor necrosis factor.";
 RT Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3].
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98414512; PubMed=9740674; DOI=10.1006/geno.1998.5407;
 RA Hurlle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
 RA "The mouse tumor necrosis factor receptor 2 gene: genomic structure and characterization of the two transcripts.";
 RT Genomics 52:79-98(1998).
 RN [4].
 RN SEQUENCE OF 1-26 FROM N.A.
 RC STRAIN=NOD;
 RA Jacob C.O., Liu J.;
 RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [5].
 RN SEQUENCE OF 1-22 FROM N.A.
 RP TISSUE=Liver;
 RA Kissingerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNFR-alpha and approximately 5-fold lower affinity for homotrimeric TNFSF1/lymphotoxin-alpha. The TRAF1/TRA2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFSF1B/TNFR2 (By similarity).
 CC -1- SUBUNIT: Binds to TRAF2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL; M60469; AAA39752.1; -;
 DR EMBL; M59378; AAA40463.1; -;
 DR EMBL; Y14619; CAA74969.1; -;
 DR EMBL; Y14620; CAA74969.1; JOINED.
 DR EMBL; Y14621; CAA74969.1; JOINED.
 DR EMBL; Y14622; CAA74969.1; JOINED.
 DR EMBL; Y14623; CAA74969.1; JOINED.
 DR EMBL; U39488; AAR85021.1; -;
 DR EMBL; X87128; CAA60618.1; -;
 DR FIR; B38634; B38634.
 DR HSSP; P19438; INCF.
 DR MGD; MGI:1314883; Tnfrsf1b.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
 DR GO; GO:0006954; P:inflammatory response; IMP.
 DR GO; GO:0008220; P:necrosis; IMP.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 4.
 DR PIRSF; PIRSF001968; TNFR_2; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00650; TNFR_NGFR_2; 3.
 KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22
 FT CHAIN 23 474 Tumor necrosis factor receptor superfamily member 1B.
 FT DOMAIN 23 258 Extracellular (Potential).

FT	TRANSMEM	259	288	Potential.
FT	DOMAIN	289	474	Cytoplasmic (Potential).
FT	REPEAT	39	77	TNFR-Cys 1.
FT	REPEAT	78	119	TNFR-Cys 2.
FT	REPEAT	120	164	TNFR-Cys 3.
FT	REPEAT	165	203	TNFR-Cys 4.
FT	DISULFID	40	54	By similarity.
FT	DISULFID	55	68	By similarity.
FT	DISULFID	58	76	By similarity.
FT	DISULFID	79	94	By similarity.
FT	DISULFID	97	111	By similarity.
FT	DISULFID	101	119	By similarity.
FT	DISULFID	121	127	By similarity.
FT	DISULFID	136	145	By similarity.
FT	DISULFID	139	163	By similarity.
FT	DISULFID	166	181	By similarity.
FT	CARBOHYD	69	69	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	195	195	N-linked (GlcNAc. .) (Potential).
FT	CONFLICT	78	78	D -> DSDTVCAD (in Ref. 3).
FT	CONFLICT	102	102	T -> S (in Ref. 3).
FT	CONFLICT	108	108	I -> T (in Ref. 3).
FT	CONFLICT	283	283	I -> F (in Ref. 3).
FT	CONFLICT	331	331	S -> SS (in Ref. 3).
FT	CONFLICT	360	360	F -> S (in Ref. 3).
FT	CONFLICT	436	436	C -> Y (in Ref. 3).
FT	SEQUENCE	474 AA; 50319 MW; 462EAE398C4D6563	CRC64;	
Query Match	26.0%;	Score 295;	DB 1;	Length 474;
Best Local Similarity	34.0%;	Pred. No. 7, 1e-17;		
Matches	66;	Conservative	24;	Mismatches 84;
				Indels 20;
				Gaps 8;
QY	8	PYASE-NOTCRDQEKYEPQHRICCSPPGTYVSAKCSIRDITVCATCAENSNEHWN	66	
Db	31	PKYPEPGYECQISQ-EYDRAQACMCAPQYVKKFCNKTSITVCADCEASMTQVWN	89	
QY	67	YLITICQLCR---PCDPVWGLEIEIAPCTSKRKTQCRQGMCA--AWALECTHCELLSDC	121	
Db	90	QFRTCLSCSSCTTDQV---EIRACTQQRNVCAEAGRYCALKTHSGRCQCNRLSKC	145	
QY	122	PPGTAEALKDEVGKNNHCVPCKAGHFQNTSPSARCPQHTRCENQGLVEAPGTAQSDT	181	
Db	146	GFGF-GVASSRAPNGVNLCKACAPTFSDTSSITDVCPRHICS-----ILAIPGNASTDA	200	
QY	182	TCKNPLEPLPPEMS	195	
Db	201	VC---APESTLS	210	
RESULT 7				
Q91ZM6				
ID	Q91ZM6	PRELIMINARY;	PRT;	433 AA.
AC	Q91ZM6;			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Tumor necrosis factor receptor type II (fragment).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RX	MEDLINE=22263089; PubMed=12376316;			
RA	Osburg B., Peiser C., Domling D., Schomburg L., Ko Y.T., Voigt K., Bickel U.;			
RA	"Effect of endotoxin on expression of TNF receptors and transport of TNF-alpha at the blood-brain barrier of the rat.";			
RT	Am. J. Physiol. Endocrinol. Metab. 283:E899-E908(2002).			
RL	EMBL; AF420214; AAL16021.1; -.			
DR	HSSP; P19438; INCF.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	Pfam; PF00020; TNFR_C6; 2.			


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DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 45723 MW; 75736DB35E72C4A CRC64;

Query Match 25.7%; Score 291.5; DB 2; Length 433;
Best Local Similarity 33.3%; Pred. No. 1.3e-16;
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASENQTCDQKEYYEYQHRICSRCPGGTYVSAAKSRIRDTVCATCAENSYNEHWY 67
DB 11 PYKPEPGNQCIQSQEYDKKQACCAKCPGGYAKHFCNKTSITVCADCAAGMFTQVWNH 70
QY 68 LTICQLC-RPC--DPVMGLEETAPCTSKRTQCRQCPGMFCA--AWALECTHCELLSDCP 122
DB 71 LHTCLSCSSCSDDQV----ETHNCTKKQNRVCACNADSYCALKHLHSGNCRQCMKLSKCG 126
QY 123 PGTEAEKDEVGKGNHNCVPCAKGHFQNTSSPASCQPHTRCENQGLVEAAGPTAQSDTT 182
DB 127 PGF-GVARSRTSNGNVICSACAPGTFSDTSTSDVCRPHRCS-----ILAIFGNASTDAV 181
QY 183 CKNPLEPLPPMSGT 197
DB 182 CASE-SPTPSAVPRT 195

RESULT 8
Q6VAU8 PRELIMINARY; PRT; 461 AA.
AC Q6VAU8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor type 2 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Inglis J.J., Chernajovsky Y., Kidd B.L.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV344841; RAQ22350.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:004872; F:receptor activity; IEA.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.
DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p...; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PIRSF; PIRSF001968; TNFR_2; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1
FT NON_TER 461
SQ SEQUENCE 461 AA; 48857 MW; B36769C080B1308A CRC64;

Query Match 25.7%; Score 291.5; DB 2; Length 461;
Best Local Similarity 33.3%; Pred. No. 1.4e-16;
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASENQTCDQKEYYEYQHRICSRCPGGTYVSAAKSRIRDTVCATCAENSYNEHWY 67
DB 25 PYKPEPGNQCIQSQEYDKKQACCAKCPGGYAKHFCNKTSITVCADCAAGMFTQVWNH 84
QY 68 LTICQLC-RPC--DPVMGLEETAPCTSKRTQCRQCPGMFCA--AWALECTHCELLSDCP 122

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FT	DISULFID	79	94	By similarity.	
FT	DISULFID	97	111	By similarity.	
FT	DISULFID	101	119	By similarity.	
FT	DISULFID	121	127	By similarity.	
FT	DISULFID	136	145	By similarity.	
FT	DISULFID	139	163	By similarity.	
FT	DISULFID	166	181	By similarity.	
FT	CARBOHYD	69	69	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	110	110	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	195	195	N-linked (GlcNac. . .) (Potential).	
SQ	SEQUENCE	474 AA;	50148 MW; 298CGAB9E8C8D714 CRC64;		
	Query Match	25.7%;	Score 291.5;	DB 1;	Length 474;
	Best Local Similarity	33.3%;	Pred. No. 1.4e-16;		
	Matches 65;	Conservative 24;	Mismatches 91;	Indels 15;	Gaps 7;
Qy	8	PYASENQTCDQGEKYEYFQHRICSCRCPPGTYYSAKCSIRIDTVCATCAENSYNHWNV	67		
Db	31	PKYPGPNQCIQSQEYDKAQMCCAKPFGQYAKHFCNKTSTDVCADCAAGMFTQWNH	90		
Qy	68	LIIQCLC-RPC--DPVMGLEIAICTSKRTQCRCPGMFCA--AWALECTHCELLSDCP	122		
Db	91	LHTCLSCSSSCSDQV----ETHNCTKKQNRVCAACNADSYCALKLSHGRCRCQMKLSKG	146		
Qy	123	PQTEAELDKVGKGNHCVCPKAGHFONTSPSARCQPHTRCENOGLEVAAPQASDPT	182		
Db	147	PGF-GVARSRTSNGNVICSACAPGTFDSTTSDTVCPRHICS----ILAIQNASITDAV	201		
Qy	183	CKNPLEPIPPPEMSGT	197		
Db	202	CASE-SPTPSAVPRT	215		

RESULT 10	
Q62327	PRELIMINARY; PRT; 459 AA.
ID	Q62327
AC	Q62327;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Tumour necrosis factor receptor 2 protein (Fragment).
DE	Name=Trnfrs1b;
GN	Mus musculus (Mouse)
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;	
[1]	SEQUENCE FROM N.A.
RN	RC STRAIN=NOD;
RC	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT	"Amino acid variation in the tumor Necrosis factor receptor 2 is
RT	linked to autoimmune diabetes in NOD mice.";
RT	Genomics 0:0-0(0).
RN	[2]
RN	SEQUENCE FROM N.A.
RP	RC STRAIN=NOD;
RC	MEDLINE=95178848; PubMed=7873884;
RA	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RX	"Allelic variation of the type 2 tumor necrosis factor receptor
RT	gene.";
RT	Mamm. Genome 5:726-727(1994).
RL	EMBL; X76401; CAA53981.1; -.
DR	PIR; I48854; I48854.
DR	HSSP; P19438; 1NCF.
DR	MGM; GGI:1314883; Trnfrs1b.
DR	GO; GO:0005615; C:extracellular space; TAS.
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:0008283; P:cell proliferation; TAS.
DR	GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
DR	GO; GO:0006954; P:inflammatory response; IMP.
DR	GO; GO:0008220; P:necrosis; IMP.
DR	InterPro; IPR001368; TNFR c6.
DR	Pfam; PF00020; TNFR c6; 2-

[illegible]


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RESULT 12
QYRL5 QYRL5 PRELIMINARY; PRT; 274 AA.
AC QYRL5;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE CD40.
GN Name=CD40;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang S., Sim G.-K.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RR EMBL; AY333789; AAP86653.1; -.
DR HSP; P25942; 1FLI.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;

Query Match 25.1%; Score 284.5; DB 2; Length 274;
Best Local Similarity 34.9%; Pred. No. 3.2e-16;
Matches 61; Conservative 18; Mismatches 89; Indels 7; Gaps 4;

QY 9 YASENOTCDQKEYEYPOHRCSSRCPTGTVSAKCSIRDTVCATCAENYHNVL 68
Db 19 YPEPTACR--EKQLVDNQ--CCNCPGKLVNDCLHTIDTECTRCQTGFELDTWNAE 74
QY 69 TTCQLCRCPDVVGLBEIEAPCTSKRTQCRQCPGMFCAAWALECTHCELLSDCPRTAE 128
Db 75 RHCHQHKYCDPLGLHVEKGTSETDTTCDEGLHCTWAA--CRSCTVHSLCPGLGVK 132
QY 129 LKDEVGKGNHCVCPKAGHFONTSSPASCQPHTRCENQGLVEAAPGTAQSDTTC 183
Db 133 -QIATGISDTICDPCPGIFGFSNVSSALEKHPWTSCTKGLVKVQAGTNKTDVIC 186

RESULT 13
TR11_MOUSE STANDARD; PRT; 625 AA.
AC Q35305; Q8VCT7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor
DE (Receptor activator of NF-kB) (Osteoclast differentiation factor
DE receptor) (ODFR).
GN Name=Trnfrs11a; Synonyms=Rank;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Caavaant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=99097247; PubMed=9878548; DOI=10.1006/bbrc.1998.9788;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANSC/OPGL; essential for
CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
CC interactions between T-cells and dendritic cells.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in
CC trabecular bone, thymus, small intestine, lung, brain and kidney.
CC Weakly expressed in spleen and bone marrow.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF019046; AAB86810.1; -;
CC EMBL; BC019185; AAB19185.1; -;
CC HSP; O14763; IDU3.
CC MGD; MGI:1314891; Tnfrsf11a.
CC GO; GO:0007275; P:development; IMP.
CC GO; GO:0007515; P:lymph gland development; IMP.
CC GO; GO:0001503; P:ossification; IMP.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 3.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 1.
CC Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
KW SIGNAL 1 30 Potential.
KW CHAIN 31 625 Tumor necrosis factor receptor
FT superfamily member 11A.
FT Extracellular (Potential).
FT TRANSMEM 215 234 Potential.
FT DOMAIN 235 625 Cytoplasmic (Potential).
FT REPEAT 35 69 TNFR-Cys 1.
FT REPEAT 72 113 TNFR-Cys 2.
FT REPEAT 115 152 TNFR-Cys 3.
FT REPEAT 155 195 TNFR-Cys 4.
FT DISULFID 35 47 By similarity.
FT DISULFID 48 61 By similarity.

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FT DISULFID 51 69 By similarity.
FT DISULFID 72 87 By similarity.
FT DISULFID 93 113 By similarity.
FT DISULFID 115 128 By similarity.
FT DISULFID 134 152 By similarity.
FT CARBOHYD 106 106 N-linked (GLNac. . .) (Potential).
FT CARBOHYD 175 175 N-linked (GLNac. . .) (Potential).
FT CONFLICT 494 494 R -> K (in Ref. 2).
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;

Query Match 25.0%; Score 283; DB 1; Length 625;

Best Local Similarity 32.6%; Pred. No. 9.6e-16;

Matches 60; Conservative 25; Mismatches 85; Indels 14; Gaps 4;

QY 4 QAVPPYASENQTCRQDEKEYEYFQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENSYN 63
DB 30 QVTPPTQTE-----RHYEHLGR-CGSRCEPGKYLGSKCTPTSDSVCLPCGPDYLD 79
QY 64 HNNYLITCOLCRPCDPVMGLEIEIAPCTSKRKTCQRCQPGMFCMAALECTHCELLSDCPP 123
DB 80 TWNEEDKLLHKVCDAGKALVAVDPGNHTAPRRCACCTAGVH---WNSDCECCRRNTECAP 136
QY 124 GTEAELEKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVBAAPGTAQSDTTC 183
DB 137 GFQAQHPQLQNK-DTVCCTPCLLGFSDVFSSTDKCKPWTNCTLLGLKLEAHQGTSDVVC 195
QY 184 KNPL 187
DB 196 SSSN 199

RESULT 14

Q86YK5 PRELIMINARY; PRT; 223 AA.

AC Q86YK5; PRT; 223 AA.
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 (Fragment).
GN Name=TNFRSF5; Synonyms=CD40;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM I).
RA He X., Xu L., Zeng Y.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY225405; AA043990.1; -.
DR HSSP; Q92956; IJMA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
FT NON_TER 223 223
SQ SEQUENCE 223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match 24.5%; Score 278; DB 2; Length 223;

Best Local Similarity 35.0%; Pred. No. 9.3e-16;

Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PPVASENQTCRQDEKEYEYFQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENSYNHNW 66

Db 22 PPTA-----CR-EKYLINSQ--CCSLCQPKQLVSDCTETETECLEPCGSEFLDTWN 72
QY 67 YLTICQLCRPCDPVMGLEIEIAPCTSKRKTCQRCQPGMFCMAALECTHCELLSDCPPTE 126
Db 73 RETHCHQHKYCDPNLGLRVQQGTSETDTICTCEBGMHCTSEA--CESCVLHRS CSPGFG 130
QY 127 ASLEKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVBAAPGTAQSDTTC 183
Db 131 VK-QIATGVSDTICEPCPGVPFSNVSSAPEKCHPWTSCETKDLVQQAQTNKTDVVC 186

RESULT 15

TNR5 HUMAN

ID TNR5 HUMAN STANDARD; PRT; 277 AA.
AC P25942; O9BYU0;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
GN Name=TNFRSF5; Synonyms=CD40;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM I).
RP MEDLINE=89356608; PubMed=2475341;
RX Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
SEQUENCE FROM N.A. (ISOFORM II).
RX MEDLINE=21117110; PubMed=11172023; DOI=10.1073/pnas.98.4.1751;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waidmann H.;
RT "Regulation of CD40 function by its isoforms generated through alternative splicing";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
RN [3]
SEQUENCE FROM N.A. (ISOFORM I), AND VARIANTS LEU-134 AND ALA-227.
RP Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Begguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.M., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RA Nature 414:865-871(2001).
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM I).
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauser R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Warra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN SEQUENCE OF 21-30.
RX PubMed=11676606; DOI=10.1006/prep.2001.1501;
RA Khandekar S.S., Silverman C., Wells-Marani J., Bacon A.M., Birrell H.,
RA Brigham-Burke M., DeMarini D.J., Jonak Z.B., Camilleri P.,
RA Fishman-Loebell J.;
RT "Determination of carbohydrate structures N-linked to soluble CD154
RT and characterization of the interactions of CD40 with CD154 expressed
RT in Pichia pastoris and Chinese hamster ovary cells.";
RL Protein Expr. Purif. 23:301-310(2001).
RN [7]
RN SEQUENCE OF 21-35.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [8]
RN INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).
RN [9]
RN INTERACTION WITH TRAF3.
RX MEDLINE=95129692; PubMed=7530216; DOI=10.1016/0014-5793(94)01406-Q;
RA Sato T., Irie S., Reed J.C.;
RT "A novel member of the TRAF family of putative signal transducing
RT proteins binds to the cytosolic domain of CD40.";
RL FEBS Lett. 358:113-118(1995).
RN [10]
RN INTERACTIONS WITH TRAF1, TRAF2, TRAF3 AND TRAF5.
RX MEDLINE=98384149; PubMed=9718306; DOI=10.1021/bi981067q;
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
RA Kehry M.R.;
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
RT interactions: regulation of CD40 signaling through multiple TRAF
RT binding sites and TRAF hetero-oligomerization.";
RL Biochemistry 37:11836-11845(1998).
RN [11]
RN INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754; DOI=10.1016/S0378-1119(97)00616-1;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.;

RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
RN [12]
RN INTERACTION WITH TRAF6.
RX MEDLINE=98095703; PubMed=9432981;
RA Kasbiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,
RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.;
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
RT extracellular signal-regulated kinase (ERK) activity in CD40 signaling
RT along a ras-independent pathway.";
RN J. Exp. Med. 187:237-244(1998).
RN [13]
RN 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RX DOI=10.1002/(SICI)1097-0134(199701)27:1<59::AID-PROT7>3.3.CO;2-Z;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [14]
RN 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RX Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
RN [15]
RN X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
RN TRAF3.
RX MEDLINE=20442386; PubMed=10984535; DOI=10.1073/pnas.97.19.10395;
RX Ni C.Z., Welsh K., Leo E., Chlou C.K., Wu H., Reed J.C., Ely K.R.;
RT "Molecular basis for CD40 signaling mediated by TRAF3.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
RN [16]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
RN TRAF3.
RX MEDLINE=22000222; PubMed=12005438; DOI=10.1016/S0969-2126(02)00733-5;
RX Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
RA Satterthwait A.C., Cheng G., Ely K.R.;
RT "Downstream regulator TANK binds to the CD40 recognition site on
RT TRAF3.";
RL Structure 10:403-411(2002).
RN [17]
RN VARIANT HIGM3 ARG-83.
RX MEDLINE=21532985; PubMed=11675497; DOI=10.1073/pnas.221456898;
RA Ferrari S., Gilliani S., Insalaco A., Al-Ghoni A., Sorresina A.R.,
RA Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,
RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
RA Plebani A.;
RT "Mutations of CD40 gene cause an autosomal recessive form of
RT immunodeficiency with hyper Igm.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
RN CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
RN CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
RN CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
RN CC secreted (isoform 2).
RN CC -!- ALTERNATIVE PRODUCTS:
RN CC Event=Alternative splicing; Named isoforms=2;
RN CC Comment=Additional isoforms seem to exist;
RN CC Name=I;
RN CC IsoId=P25942-1; Sequence=Displayed;
RN CC Name=II;
RN CC IsoId=P25942-2; Sequence=VSP_006472, VSP_006473;
RN CC -!- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
RN CC -!- DISEASE: Defects in TNFSF5 are the cause of hyper-Igm
RN CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an

Query Match 24.5%; Score 278; DB 1; Length 277;
Best Local Similarity 35.0%; Pred. NO. 1.2e-15;
Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

Qy	7	PPYASENQTCRDOEKYEYEPQHRITCCSRCPGTTVSAKSRIRDTVTCATCAENSNEYHNH	66
Db	22	PPTA-----CR--EKQYLINSQ--CCSLCPQGGKLVSDCTEFTEFTECLPCGSESEFLDTWN	72
Qy	67	YLTIQLCHRPCDPVWGLEBEIAPCTSKRKYTCRCQPGMFCAAWALECTHCELLSDCPGTE	126
Db	73	RETHCHQHKYCDPNLGLRVQOGKTSFETDITCTCEGWHCTSEA--CESCVLHRS CSPGFG	130
Qy	127	ASLKBVEGVGNHNVCPKAGHFQNTSSPSARCQPHITCENQGLVEAAPGTAQSDTTC	183
Db	131	VK-QIATGVSDTITCBFCVPVGFNSVSAFEKCHPWTSCETKDLVQOAGTKTDVVC	186

Search completed: September 23, 2005, 10:30:34
Job time : 177 secs

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